

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:57:44 ; Search time 9057 Seconds

(without alignments)  
11251.993 Million cell updates/sec

Title: US-08-917-710-1

Perfect score: 2155

Sequence: 1 CGGCGGCCGCCGCTCTAGAA.....CTAATAAAAAAAAAAAAAA 2155

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pac.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_srs.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2043.2	94.8	2063	9	AF538734 Homo sapi
2	1869.2	86.7	1976	9	AF538732 Homo sapi
3	1848.2	85.8	1857	9	AF167343 Homo sapi
4	1538.8	71.4	1561	9	BC053621 Homo sapi
5	1242.8	57.7	4724	9	AB006537 Homo sapi
6	1242.8	57.7	4726	6	CO715161 Homo sapi
7	1096.6	50.9	4575	9	AF538730 Homo sapi
8	1068.8	49.6	4637	9	AF538733 Homo sapi
9	1056.8	49.0	1740	6	AR166115 Sequence
10	1056.8	49.0	1740	6	AR166115 Sequence
11	1047.8	48.6	1713	6	AX616663 Sequence
12	1047.8	48.6	2064	6	AX704564 Sequence
13	1043	48.4	2733	6	BD311181 Antagonis
14	1043	48.4	2733	6	CO796431 Sequence
15	1043	48.4	2733	6	AR442283 Sequence
16	1020.8	48.4	2733	6	AX503601 Sequence
17	1020.8	47.3	1822	9	AY182233 Macaca fa
18	1019.2	47.3	1822	9	AY182234 Macaca mu
19	935	43.4	3080	9	AF167340 Homo sapi

20	930.2	43.2	184203	9	AC008249 Homo sapi
21	922.6	42.8	4488	9	AF538731 Homo sapi
22	891.8	41.4	1916	10	BC021159 Mus muscu
23	794.2	36.9	3355	6	AR166116 Sequence
24	794.2	36.9	3355	6	AX683050 Sequence
25	794.2	36.9	3355	10	MM1LRACP X85999 M. musculus
26	790.2	36.7	2058	6	AX704566 Sequence
27	783	36.3	1862	10	RN448592 Rattus norv
28	595.8	27.6	601	11	BV184131 Bqmt1.4321
29	447	20.7	1408	5	CR353678 Gallus ga
30	447	20.7	1456	5	BX936140 Gallus ga
31	442.8	20.5	642	10	AB079119 Rattus no
32	367.4	17.0	443	6	AX410972 Sequence
33	281.2	13.5	880	6	AF167333S04 AF167336 Homo sapi
34	285.4	13.2	287	6	CO078673 Sequence
35	285.4	13.2	287	6	CO078673 Sequence
36	249.4	11.6	16161	2	AC119283 Mus muscu
37	246.6	11.4	272085	2	AC098400 Rattus no
38	232.8	10.8	729	11	BV019633 S212P6158
39	223.6	10.4	271	6	AX410606 Sequence
40	218.4	10.1	478	6	CO069416 Sequence
41	218.4	10.1	478	6	CO069416 Sequence
42	199	9.2	548	9	AF016261 Homo sapi
43	199	9.2	594	9	AF167337 Homo sapi
44	168	7.8	311	9	AF167338 Homo sapi
45	167.4	7.8	169	6	CO058471 Sequence

## ALIGNMENTS

RESULT 1	AF538734	2063 bp	mRNA	linear	PRI 28-JUL-2003
LOCUS	AF538734				
DEFINITION	Homo sapiens clone L2 soluble interleukin-1 receptor accessory				
ACCESSION	AF538734				
VERSION	AF538734.1	GI:33286880			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Jensen, L.E. and Whitehead, A.S.				
TITLE	Expression of alternatively spliced interleukin-1 receptor accessory protein mRNAs is differentially regulated during inflammation and apoptosis				
JOURNAL	Cell. Signal. 15 (8), 793-802 (2003)				
MEDLINE	22664804				
PUBMED	12781872				
REFERENCE	2 (bases 1 to 2063)				
AUTHORS	Jensen, L.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-AUG-2002) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104-6084, USA				
FEATURES					
source	1..2063				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="L2"				
	/cell_line="HepG2"				
5'UTR	1..206				
misc_feature	118..119				
	/note="alternative splice site for exon 1 and exon 2"				
misc_feature	205..206				
	/note="alternative splice site for exon 2 and exon 3"				
CDS	207..1277				
	/note="stop-1RACp; alternatively spliced"				
	/codon_start=1				
	/product="soluble interleukin-1 receptor accessory				



DB 1860 TTTAAACACTATNGTCAATATTTTACAGAGGTTTATATATACACGACCAATTGCT 1919

QY 2016 AAAAAGAAATCATTTAAATTTATGATTTTAAATGATATACATGATTTCTATGTGATA 2015

DB 1920 AAAAAGAAATCATTTAAATTTATGATTTTAAATGATATACATGATTTCTATGTGATA 1979

QY 2076 GTACATATATTTATTTACATTAATGAAATATTAATAAGCCTTCTGTGAGAGTGCTGCTC 2135

DB 1980 GTACATATATTTATTTCTACATTAATGAAATATTAATAAGCCTTCTGTGAGAGTGCTGCTC 2039

QY 2136 CTAATAAAAAAAAAAAAAA 2155

DB 2040 CTAATAAAAAAAAAAAAAA 2059

RESULT 2

AF538732 1976 bp mRNA linear PRI 28-JUL-2003

LOCUS AF538732

DEFINITION Homo sapiens clone L1 soluble interleukin-1 receptor accessory protein mRNA, complete cds; alternatively spliced.

ACCESSION AF538732

VERSION AF538732.1 GI:33286876

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1976) Jensen, L.E. and Whitehead, A.S. Expression of alternatively spliced interleukin-1 receptor accessory protein mRNAs is differentially regulated during inflammation and apoptosis

REFERENCE 2 (bases 1 to 1976) Jensen, L.E. Direct Submission

JOURNAL Submitted (19-AUG-2002) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104-6084, USA

MEDLINE 12781872

PUBMED 22664804

AUTHORS

TITLE

FEATURES

source location/Qualifiers

1..1976

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="L1"

/cell\_line="HepG2"

1..119

118..119

/note="alternative splice site for exon 1 and exon 3"

CDS 120..1190

/note="5'UTR; alternatively spliced"

/codon\_start=1

/product="soluble interleukin-1 receptor accessory protein"

/protein\_id="AA001757.1"

/db\_xref="GI:33286877"

/translation="MTLMCVSLYFYGILOSASERCDMDGLTMKQIOVFEDDEPAR IKCPLEHLEKFNYSSTAAGLTLIWTRODRDLERINFLPENRISKEKVTLMR PTLINDGNTYOMLNTYCSKVAFLPDEVGKSCFNSPMKLVPKLYIEGYORIC NVDSGPSVSKPTITWAGCYKIONENNV BEGNLSFLALISNNKNGICVITYE NGRPHLRITLTVKVGSPRNAVPVTHSPMDHYVERKEPEELLICTVYFSLIMS RNEWTWITDKKPDITITDVITNESISHSRTEDETRIQIISIKKVTSEDLKRSTVCHA RSKAGEVAKAKVKQKGRGQ"

misc\_feature 1170..1171

/note="alternative splice site for exon 9 and exon 10"

3'UTR 1191..1954

polyA\_signal 1910..1915

ORIGIN

Query Match 86.7%; Score 1869.2; DB 9; Length 1976;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 1969; Conservative 0; Mismatches 3; Indels 88; Gaps 1;

QY 96 TGGCGGATCCAGAGTCTCCGCGGGGTCCGCTTTGGCCAGAGGCGGGAGAGAGAGGCGCC 155

DB 1 TGGCGGATCCAGAGTCTCCGCGGGGTCCGCTTTGGCCAGAGGCGGGAGAGAGAGGCGCC 60

QY 156 GCGACACTGACACCCATCCCGGCTGCTTTGCTGGCCGCCCTCTGAGCTTCCAGAAAGGC 215

DB 61 GCGACACTGACACCCATCCCGGCTGCTTTGCTGGCCGCCCTCTGAGCTTCCAGAG----- 114

QY 216 ATGTCATGTGATCATCATCTAAAGAACTGACATGACAGAGGCCCTTAGAGGCTCATC 275

DB 115 ----- 114

QY 276 TTGGCCCTCCCTTAATATCTCAAGAGATGACACTCTGAGTGATGATGAGTCTCTAC 335

DB 115 -----AAGAGTACACTTCTGTGTGTGTGATGATGATCTCTAC 152

QY 336 TTTTATGAAATCTCGAAGATGATGCTCGAAGACGCTCGATGATGAGGAGACTAGACACC 395

DB 153 TTTTATGAAATCTCGAAGATGATGCTCGAAGACGCTCGATGATGAGGAGACTAGACACC 212

QY 396 ATGAGCAATTCAGATGTTTGAAGATGAGCCAGCTCGATCAAGTCCCACTCTTGA 455

DB 213 ATGAGCAATTCAGATGTTTGAAGATGAGCCAGCTCGATCAAGTCCCACTCTTGA 272

QY 456 CACTTCTGAAATTCAGATGATGACAGACAGCCATTCAGTGGCTTACTCTGATCTGTAT 515

DB 273 CACTTCTGAAATTCAGATGATGACAGACAGCCATTCAGTGGCTTACTCTGATCTGTAT 332

QY 516 TGGACTGAGAGACCGGAGCCTTGAGAGCCATTAATCTCGGCTCCCGAGAACCGC 575

DB 333 TGGACTGAGAGACCGGAGCCTTGAGAGCCATTAATCTCGGCTCCCGAGAACCGC 392

QY 576 ATTAGTAGAGAGAGATGCTGTGCTCCGCGCCAGCTCTCTCATGATGACATGAGCAAC 635

DB 393 ATTAGTAGAGAGAGATGCTGTGCTCCGCGCCAGCTCTCTCATGATGACATGAGCAAC 452

QY 636 TATACCTGATGTTAAGAACACTATATTCAGAGAAAGTTGATTTCCCTTGAAGTT 695

DB 453 TATACCTGATGTTAAGAACACTATATTCAGAGAAAGTTGATTTCCCTTGAAGTT 512

QY 696 GTTCAAAAAAGACGCTGTTCAATTCGCCCATGAACTCCCATGATGATTAACGTGTATA 755

DB 513 GTTCAAAAAAGACGCTGTTCAATTCGCCCATGAACTCCCATGATGATTAACGTGTATA 572

QY 756 GAATATGACATTCAGAGATCACTTGTCCAAATGATGATGATTTTCTTCCAGTGTC 815

DB 573 GAATATGACATTCAGAGATCACTTGTCCAAATGATGATGATTTTCTTCCAGTGTC 632

QY 816 AAACCGATATCACTTGTATATGAGGCTGTATATAATACAGATTTTATAATGTAATA 875

DB 633 AAACCGATATCACTTGTATATGAGGCTGTATATAATACAGATTTTATAATGTAATA 692

QY 876 CCCGAGGTATGAACTGAGTTTCTCATTTGCTTAATTTCAATATGAAATTCACACA 935

DB 693 CCCGAGGTATGAACTGAGTTTCTCATTTGCTTAATTTCAATATGAAATTCACACA 752

QY 936 TGTGTTGTTACATATCAAGAAAATGAGAGCTGATCTCATCAACAGACTGTGACTGA 995

DB 813 TGTGTTGTTACATATCAAGAAAATGAGAGCTGATCTCATCAACAGACTGTGACTGA 872

QY 996 AAGGTGATGAGCTGCTCAAAAAATGAGAGCCCGCTGATCAATCACTCACTATGATCAT 1055

DB 813 AAGGTGATGAGCTGCTCAAAAAATGAGAGCCCGCTGATCAATCACTCACTATGATCAT 872

QY 1056 GTGCTATGAGAAAGACAGAGAGAGAGACTATTCCTGTAACGCTATTTTAAGT 1115

DB 873 GTGCTATGAGAAAGACAGAGAGAGAGACTATTCCTGTAACGCTATTTTAAGT 932

QY 1116 TTTCTGATGATTTCTGCAATGAGTTTGTGTGACCATTTGATGAGAAAAAACCCTGATGAC 1175

DB 933 TTTCTGATGATTTCTGCAATGAGTTTGTGTGACCATTTGATGAGAAAAAACCCTGATGAC 992



Db 241 GAGCCAAATTAATCTCCGCTCCCGAGAACCGCATTAAGTAAAGAAAGATGTGCTGG 300  
Qy 603 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTAGGAAACTAC 662  
Db 301 TTCGGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGATGTAGGAAACTAC 360  
Qy 663 TAATGAGCAAAAGTTGCAATTCCTGGAAGTTGTCCAAAAGACAGCTGTTTCATTC 722  
Db 361 TAATGAGCAAAAGTTGCAATTCCTGGAAGTTGTCCAAAAGACAGCTGTTTCATTC 420  
Qy 723 CCCAAGAACTCCGAGTGAATACTGTATATAGTAATGGCATTCAGAGATCACTTGT 782  
Db 421 CCCAAGAACTCCGAGTGAATACTGTATATAGTAATGGCATTCAGAGATCACTTGT 480  
Qy 783 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCACTATGCACTTGTATATGGC 842  
Db 481 CCAATGTAGATGATATTTTCTTCCAGTGTCAACCGCACTATGCACTTGTATATGGC 540  
Qy 843 TGTATTAATATACAAATTTTATATATGATATACCGAAGGTATCACTTGAGTTCTC 902  
Db 541 TGTATTAATATACAAATTTTATATATGATATACCGAAGGTATCACTTGAGTTCTC 600  
Qy 903 ATGACCTTAATTTCAATTAATGAAATTAACATGTGTTGTACATATCCAGAAATGA 962  
Db 601 ATGACCTTAATTTCAATTAATGAAATTAACATGTGTTGTACATATCCAGAAATGA 660  
Qy 963 CGTACGTTTCATCTGACGAGACTCTGACTGTAAGGTATGAGGCTCTCCAAAATGCA 1022  
Db 661 CGTACGTTTCATCTGACGAGACTCTGACTGTAAGGTATGAGGCTCTCCAAAATGCA 720  
Qy 1023 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTATGAGAAAGACCGAGAG 1082  
Db 721 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGCTATGAGAAAGACCGAGAG 780  
Qy 1083 GAGCTACTCATTCCTGTACGCTATTTAGTTTCTGATGATGATCTCGCAATGAGGT 1142  
Db 781 GAGCTACTCATTCCTGTACGCTATTTAGTTTCTGATGATGATCTCGCAATGAGGT 840  
Qy 1143 TGTGTGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTACCATTAAC 1202  
Db 841 TGTGTGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTACCATTAAC 900  
Qy 1203 AGTATAGTCATATAGTAAGCAAGATGAACTAGAACTGAGATGAGCATCAAGAA 1262  
Db 901 AGTATAGTCATATAGTAAGCAAGATGAACTAGAACTGAGATGAGCATCAAGAA 960  
Qy 1263 GTTACCTCTGAGAGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTCCAA 1322  
Db 961 GTTACCTCTGAGAGATCTCAAGCGCAGCTATGTCTGTCAATGCTAGAAAGTCCAA 1020  
Qy 1323 GTTGTGCAAGCAAGCAAGGTATGAGCAAGAAAGTATAGTCCGTCATGATGATCTCT 1382  
Db 1021 GTTGTGCAAGCAAGCAAGGTATGAGCAAGAAAGTATAGTCCGTCATGATGATCTCT 1080  
Qy 1383 CAGCTCCAAATTAATCATTTGTGTGATAGCAAAAGAGATTTGAGAAAGAGAGC 1442  
Db 1081 CAGCTCCAAATTAATCATTTGTGTGATAGCAAAAGAGATTTGAGAAAGAGAGC 1140  
Qy 1443 TCCAGCACTGAGCTGAGGCACTTCAACCATAGTATGATCAAACTTAAATGAAAAAT 1502  
Db 1141 TCCAGCACTGAGCTGAGGCACTTCAACCATAGTATGATCAAACTTAAATGAAAAAT 1200  
Qy 1503 ATGAAAGTTTCATCTATATAGTAACTCAAAATTTGTTCTGATATTTGTTAGACGT 1562  
Db 1201 ATGAAAGTTTCATCTATATAGTAACTCAAAATTTGTTCTGATATTTGTTAGACGT 1260  
Qy 1563 AATGCCCAATGTAGCTTAAAAAATCGAGTATGACATGAGACAAATTTTGTCTG 1622  
Db 1261 AATGCCCAATGTAGCTTAAAAAATCGAGTATGACATGAGACAAATTTTGTCTG 1320  
Qy 1623 TACATTTATGAAAAATTAATAAAGAAATATATCAAGGTACCAAGATGAGAAAAAC 1682

Db 1321 TACATTTATGAAAAATTAATAAAGAAATATATCAAGGTACCAAGATGAGAAAAAC 1380  
Qy 1683 TGTATAGGACCACTATTTGTTGTAATTTATTAAGACCTTTTAAAAATCATGATGAG 1742  
Db 1381 TGTATAGGACCACTATTTGTTGTAATTTATTAAGACCTTTTAAAAATCATGATGAG 1440  
Qy 1743 AGTTAAGATCATAAAAAAGTTGATCATCTGACCTTAAGACTTTCCGAAATTTCTCG 1802  
Db 1441 AGTTAAGATCATAAAAAAGTTGATCATCTGACCTTAAGACTTTCCGAAATTTCTCG 1500  
Qy 1803 AACCAATTAAGAAAGGAAATTAATACCTTTAATTAATTAATGAGCACTATCTGAGT 1862  
Db 1501 AACCAATTAAGAAAGGAAATTAATACCTTTAATTAATTAATGAGCACTATCTGAGT 1560  
Qy 1863 TGTAAACATTTAATTAAGACCACTCAATTTGATGACAACTAATTAAGTATGAAATG 1922  
Db 1561 TGTAAACATTTAATTAAGACCACTCAATTTGATGACAACTAATTAAGTATGAAATG 1620  
Qy 1923 TTAATTTCCAAAATGATATTAATTAATTAATTTAAACATGATATCAATTTAAAG 1982  
Db 1621 TTAATTTCCAAAATGATATTAATTAATTAATTTAAACATGATATCAATTTAAAG 1680  
Qy 1983 CAGGTTATATATACAGACGACCAATGCTAAATGAAATCATTAATTAATGATG 2042  
Db 1681 CAGGTTATATATATACAGACGACCACTAATTTGAAATCATTTAATTAATGATG 1740  
Qy 2043 TTAATGTATATACATGATTTCTATGTTGATAGTACTATATTAATTTCAATTAATG 2102  
Db 1741 TTAATGTATATACATGATTTCTATGTTGATAGTACTATATTAATTTCAATTAATG 1800  
Qy 2103 AATTATTAAGCTCTTCTTGACAGAGTGTCTCTCTTAAAAAATTTTTAAAAA 2155  
Db 1801 AATTATTAAGCTCTTCTTGACAGAGTGTCTCTCTTAAAAAATTTTTAAAAA 1853

RESULT 4  
BC053621  
LOCUS  
DEFINITION  
Homo sapiens interleukin 1 receptor accessory protein, transcript variant 2, mRNA (cDNA clone MGC:61532 IMAGE:6160894), complete cds.  
ACCESSION  
BC053621  
VERSION  
BC053621.1 GI:31565480  
KEYWORDS  
MGC.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 1561)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Burow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldo, K.F., Caesvar, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettleman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1561)  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
DIRECT Submission  
Straussberg, R.

JOURNAL

Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNI)  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
Akhter, N., Ayala, K., Beckert, S., Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastaglio, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantir, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., H. and Green, B.D.

FEATURES  
source  
1..1561  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="MGC:61532 IMAGE:6160894"  
/tissue\_type="Skin, melanotic melanoma."  
/clone\_id="Nih MGC\_72"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
1..1561  
/gene="IL1RAP"  
/note="synonyms: IL-1RAP, IL1R3"  
/db\_xref="locusid:3556"  
/db\_xref="MIM:602626"  
211..1281  
/gene="IL1RAP"  
/codon\_start=1  
/product="interleukin 1 receptor accessory protein,  
isoform 2"  
/protein\_id="AAH3621.1"  
/db\_xref="GI:31565481"  
/db\_xref="locusid:3556"  
/db\_xref="MIM:602626"  
/translation="MTLMCVSLVLYFYLQSDASERCDDMDLTMKQIOVDEDEPAR  
IKCPLEHLEKFNSTASAGLTLIWTRODRLERINRLPENRISKEVDLNR  
PLINDNGNTCMKNTYVGSKVAFLPEVQKSCSPMPLPVKLIYRGIORIC  
PNVDYFSSVKEPTITWMCYKTONRNVTPEGMNLSEILALISNNGTCAVTVYE  
NGRTFHLTRTLIVKVSFKNAVPVHSPVDHVEPEPEELITCTYFSTLMS  
NBEVMTIDGKKPDITIDVTINISHSRTEDETRTQIUSIKKVTSEDEKRSYCHA  
RSAGEVAKAAKVKQKXNRGCGO"

gene

CDS

1..1561  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="MGC:61532 IMAGE:6160894"  
/tissue\_type="Skin, melanotic melanoma."  
/clone\_id="Nih MGC\_72"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
1..1561  
/gene="IL1RAP"  
/note="synonyms: IL-1RAP, IL1R3"  
/db\_xref="locusid:3556"  
/db\_xref="MIM:602626"  
211..1281  
/gene="IL1RAP"  
/codon\_start=1  
/product="interleukin 1 receptor accessory protein,  
isoform 2"  
/protein\_id="AAH3621.1"  
/db\_xref="GI:31565481"  
/db\_xref="locusid:3556"  
/db\_xref="MIM:602626"  
/translation="MTLMCVSLVLYFYLQSDASERCDDMDLTMKQIOVDEDEPAR  
IKCPLEHLEKFNSTASAGLTLIWTRODRLERINRLPENRISKEVDLNR  
PLINDNGNTCMKNTYVGSKVAFLPEVQKSCSPMPLPVKLIYRGIORIC  
PNVDYFSSVKEPTITWMCYKTONRNVTPEGMNLSEILALISNNGTCAVTVYE  
NGRTFHLTRTLIVKVSFKNAVPVHSPVDHVEPEPEELITCTYFSTLMS  
NBEVMTIDGKKPDITIDVTINISHSRTEDETRTQIUSIKKVTSEDEKRSYCHA  
RSAGEVAKAAKVKQKXNRGCGO"

ORIGIN

Query Match 71.4%; Score 1538.8; DB 9; Length 1561;  
Best Local Similarity 99.5%; Pred. No. 1.1e-310;  
Matches 1554; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 92 AGACGCGCGGATCCAGGTCCTCCGGGTCCTGTTGGCCAGAGCGCGGAGAGAGAGT 151  
Db 1 AGACGCGCGGATCCAGGTCCTCCGGGTCCTGTTGGCCAGAGCGCGGAGAGAGAGT 60  
QY 152 GCGCGCGGACACTGACCCCATCCCGGCTGCTTTGCTCGGCCCTTCTGCTTCCAGAA 211  
Db 61 GCGCGCGGACACTGACCCCATCCCGGCTGCTTTGCTCGGCCCTTCTGCTTCCAGAA 120

QY 212 AGGCATGCGCATGTGATGATCACTAAGAACTAGAAAGTCCAGAGCCCTTGAAGGCTC 271  
Db 121 AGGCATGCGCATGTGATGATCACTAAGAACTAGAAAGTCCAGAGCCCTTGAAGGCTC 179  
QY 272 ACTCTGCCCCCTCCCTTTAATCTCAAGATGACACTTGTGTGTGTGTGTGTGTGTGT 331  
Db 180 ACTCTGCCCCCTCCCTTTAATCTCAAGATGACACTTGTGTGTGTGTGTGTGTGTGT 239  
QY 332 CTAATTTTATGAAATCTGCAAGATGAGGCTTCAAGAGGCTGAGTGTGAGGCTGAG 391  
Db 240 CTAATTTTATGAAATCTGCAAGATGAGGCTTCAAGAGGCTGAGTGTGAGGCTGAG 299  
QY 392 CACCATGAGGCAAAATCCAAATGTTTGAAGATGAGGAGCTGAGTCAAGATGAGGCTG 451  
Db 300 CACCATGAGGCAAAATCCAAATGTTTGAAGATGAGGAGCTGAGTCAAGATGAGGCTG 359  
QY 452 TGAACACTTCTTGAATTTAATTAAGCAAGCAAGCCCTTCACTGCTGCTGCTGCTG 511  
Db 360 TGAACACTTCTTGAATTTAATTAAGCAAGCAAGCCCTTCACTGCTGCTGCTGCTG 419  
QY 512 GTATTGACTAAGCAGGACCGGACCTTGAAGGCAATTAATCTTCCGCTCCCGAGAA 571  
Db 420 GTATTGACTAAGCAGGACCGGACCTTGAAGGCAATTAATCTTCCGCTCCCGAGAA 479  
QY 572 CCGCATTAAGAGAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 631  
Db 480 CCGCATTAAGAGAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539  
QY 632 CAACATTAAGAGAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 691  
Db 540 CAACATTAAGAGAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599  
QY 692 AGTTGTTCAAAAAGACAGCTGTTTCAATCCCCCATGAACTCCAGTGCATTAATCTGA 751  
Db 600 AGTTGTTCAAAAAGACAGCTGTTTCAATCCCCCATGAACTCCAGTGCATTAATCTGA 659  
QY 752 TATAGAAATGCGATTCAGAGATCACTGTGCAAAATGAGATGATTTTCCCTTCAG 811  
Db 660 TATAGAAATGCGATTCAGAGATCACTGTGCAAAATGAGATGATTTTCCCTTCAG 719  
QY 812 TGTCAAAAGCACTATCATCTGTATATGAGGCTGTATTAATAATCAAGATTTTATATGT 871  
Db 720 TGTCAAAAGCACTATCATCTGTATATGAGGCTGTATTAATAATCAAGATTTTATATGT 779  
QY 872 AATACCGAAGGTATGAACTTGAATTTCTCTCATTTGCTTAATTTCAATTAATGAATTA 931  
Db 780 AATACCGAAGGTATGAACTTGAATTTCTCTCATTTGCTTAATTTCAATTAATGAATTA 839  
QY 932 CACATGTTGTTATCATATCCAGAAATGAGAGTTCATCTCACAGAGACTCTGAC 991  
Db 840 CACATGTTGTTATCATATCCAGAAATGAGAGTTCATCTCACAGAGACTCTGAC 899  
QY 992 TGTAAAGTAGTAGGCTCTCCAAAATGAGAGTCCCTGTGATCATTCCTTAATGA 1051  
Db 900 TGTAAAGTAGTAGGCTCTCCAAAATGAGAGTCCCTGTGATCATTCCTTAATGA 959  
QY 1052 TCAATGAGTCTATGAGAAAGAACCGAGAGAGAGTCACTTCCCTGAGAGGCTTATTT 1111  
Db 960 TCAATGAGTCTATGAGAAAGAACCGAGAGAGAGTCACTTCCCTGAGAGGCTTATTT 1019  
QY 1112 TAGTTTCTGATGATTTCTGCAATGAGTTTGTGAGACATTTGAGAAAAAACTGGA 1171  
Db 1020 TAGTTTCTGATGATTTCTGCAATGAGTTTGTGAGACATTTGAGAAAAAACTGGA 1079  
QY 1172 TGAACATCAATTAAGTATGACCATTAAGCAAAAGTATAGTCAATTAAGTATGAAGATGA 1231  
Db 1080 TGAACATCAATTAAGTATGACCATTAAGCAAAAGTATAGTCAATTAAGTATGAAGATGA 1139  
QY 1232 AACTAGAACTGAGATTTTGAAGATCAAGAAATTAATCTGAGATTTCTCAAGGAGCTA 1291  
Db 1140 AACTAGAACTGAGATTTTGAAGATCAAGAAATTAATCTGAGATTTCTCAAGGAGCTA 1199

QY 1292 TGTCTGTCATGCTAGAGAGTGCACAAAGCGAAGTTGCCAAAGACGCAAGTGAAGACGAA 1351  
 Db 1200 TGTCTGTCATGCTAGAGAGTGCACAAAGCGAAGTTGCCAAAGACGCAAGTGAAGACGAA 1259  
 QY 1352 AGGTATATGATGCGGTCAGTGTGATCTCTCAGCTCCAAATTAATCATTTGTGTGATTA 1411  
 Db 1260 AGGTATATGATGCGGTCAGTGTGATCTCTCAGCTCCAAATTAATCATTTGTGTGATTA 1319  
 QY 1412 GGCACAAAAGAGAGATTGAGAACAAAGAGCTCCAGCACTAGCCTGAACGATCTAAC 1471  
 Db 1320 GGCACAAAAGAGAGATTGAGAACAAAGAGCTCCAGCACTAGCCTGAACGATCTAAC 1379  
 QY 1472 CATATGATATGATCAACTTAATGAAATAATGTAAGTTTCATCTATGTAAGTATCTC 1531  
 Db 1380 CATATGATATGATCAACTTAATGAAATAATGTAAGTTTCATCTATGTAAGTATCTC 1439  
 QY 1532 AAAATATGTTTCTGATATTTGTTAGTACCGTAAATCCCAATGTAGCTAAAAATCGAC 1591  
 Db 1440 AAAATATGTTTCTGATATTTGTTAGTACCGTAAATCCCAATGTAGCTAAAAATCGAC 1499  
 QY 1592 GGTAGTACAGTACAGACAAATTTGTGTCTGTACAAATTAATGAAATTAATTAACAAAGAA 1651  
 Db 1500 GGTAGTACAGTACAGACAAATTTGTGTCTGTACAAATTAATGAAATTAATTAACAAAGAA 1559  
 QY 1652 AA 1653  
 Db 1560 AA 1561

RESULT 5  
 LOCUS AB006537 4724 bp mRNA linear PRI 09-APR-1998  
 DEFINITION Homo sapiens mRNA for interleukin 1 receptor accessory protein, complete cds.

ACCESSION AB006537  
 VERSION AB006537.1 GI:3041772  
 KEYWORDS interleukin 1 receptor accessory protein.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (sites)  
 Saito, T. and Seki, N.  
 Molecular cloning of human interleukin 1 receptor accessory protein  
 Unpublished  
 2 (bases 1 to 4724)  
 Saito, T.  
 Direct Submission  
 Submitted (12-AUG-1997) Yoshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group, Anagawa 4-9-1, Inage, Chiba 263, Japan (E-mail: t\_saito@nirs.go.jp, Tel: 043-206-3195, Fax: 043-251-9818)

FEATURES  
 source  
 1..4724  
 location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="brain"  
 /dev\_stage="fetal"  
 207..1919  
 /codon\_start=1  
 /product="interleukin 1 receptor accessory protein"  
 /protein\_id="BA25421.1"  
 /db\_xref="GI:3041773"  
 /translation="MTLLMVCVSLTFYGILOSASERCDMDGLPTMRQIQVFEDEPAR  
 IKCPLEHRLKENVSTASAGLTIWYTRQDRDLEBINFRLPENRISKEDIMTR  
 PLTNDNTYMLNTTYCSKVAFLVWQKDSCEFNPKMLPKLYIEGIDRITC  
 PNVDYPRSSVYPTITWYMGCKTIONRNNUYBEGNISFLIALISNNQNCVYTVB  
 NKRTHLRLTLTKVVGSKNVPVISHSPNDHVEYKEPEBELIPCTVYFSLMS  
 RNEVWITIDGRKPDITIDVNTINISISRDETRTILSIKVTSDRLKSYCHA  
 RSKAGEVAAAKQKVPAPRYVELACGATVLLVILIVVHAVYMLEVNLVYRAH  
 FGTDETLIDGKEIDIVYSYARAEEBEVLLTRGLVLENGYKCTIFDRSLGGIV  
 TDETLISIQSRRLVLPVNPVLTGQALTELKAGLENMASRGINIVILVYKAVE

ORIGIN  
 polyA\_site  
 TRKRELKRAKTVTLVKKKGEKSKYRQGRFVKQLQVAMPVKKSPPRSSDDBOGLSYSS  
 LKNV  
 4724  
 /note="28 a nucleotides"

Query Match 57.7%; Score 1242.8; DB 9; Length 4724;  
 Best Local Similarity 99.8%; Pred. No. 7e-249; Indels 1; Gaps 1;  
 Matches 1255; Conservative 0; Mismatches 2

QY 96 TGCCGGGATCCAGGTCCTCCGGGGTCGCTTTGGCCAGAGGCGCGGAAGAGAGTGC 155  
 Db 1 TGCCGGGATCCAGGTCCTCCGGGGTCGCTTTGGCCAGAGGCGCGGAAGAGAGTGC 60  
 QY 156 GGGACACTGCACCCATCCCGGCTGCTTTTGTCTGCGGCCCTCTCACTTCCAGAAAGGC 215  
 Db 61 GGGACACTGCACCCATCCCGGCTGCTTTTGTCTGCGGCCCTCTCACTTCCAGAAAGGC 120  
 QY 216 ATCGTCATGATCATCACTTAAGAACTAAGACATGACAGGCGCTTAGAGCTCACTC 275  
 Db 121 ATCGTCATGATCATCACTTAAGAACTAAGACATGACAGGCGCTTAGAGCTCACTC 179  
 QY 276 TTGCCCCCTCCTTATATATCTCAAGAGATGACCTTGTGTGTGTAGTGTCTTAC 335  
 Db 180 TTGCCCCCTCCTTATATATCTCAAGAGATGACCTTGTGTGTGTAGTGTCTTAC 239  
 QY 336 TTTTATGGAATCCGCGAAAGTGAATGCTCGAGAGCGTGGAGATGAGGGACTAGACAC 395  
 Db 240 TTTTATGGAATCCGCGAAAGTGAATGCTCGAGAGCGTGGAGATGAGGGACTAGACAC 239  
 QY 396 ATGAGCAATCCAGAGTGTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 455  
 Db 300 ATGAGCAATCCAGAGTGTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 359  
 QY 456 CACTTCTGTAATTAATCACTACAGACAGCCCATTTGAGCTTGCTTACTGTCTGTAT 515  
 Db 360 CACTTCTGTAATTAATCACTACAGACAGCCCATTTGAGCTTGCTTACTGTCTGTAT 419  
 QY 516 TGACACTAGACAGACCGGACCTTGAGGAGCCCAATTAATTCGCGCTCCCGAGAACCG 575  
 Db 420 TGACACTAGACAGACCGGACCTTGAGGAGCCCAATTAATTCGCGCTCCCGAGAACCG 479  
 QY 576 ATTAGTAGAGAAAGATGT 635  
 Db 480 ATTAGTAGAGAAAGATGT 539  
 QY 636 TATACCTGCACTGTTAAGGAACACTACATATGAGGAAAGTTCATTCCTCGTGAAGTT 695  
 Db 540 TATACCTGCACTGTTAAGGAACACTACATATGAGGAAAGTTCATTCCTCGTGAAGTT 599  
 QY 696 GTTCAAAAAGACAGCTGTTTCAATTCGCCCATGAACTCCAGTGCATAAAGTGTATTA 755  
 Db 600 GTTCAAAAAGACAGCTGTTTCAATTCGCCCATGAACTCCAGTGCATAAAGTGTATTA 659  
 QY 756 GAATATGCACTTCAAGAGACACTTGTCCAAAGTGAATGATATTTCCCTCCAGTGC 815  
 Db 660 GAATATGCACTTCAAGAGACACTTGTCCAAAGTGAATGATATTTCCCTCCAGTGC 719  
 QY 816 AAACCGACTATCACTGTGTATATGAGCTGTATTAATAATCAGAAATTTAATAATGATA 875  
 Db 720 AAACCGACTATCACTGTGTATATGAGCTGTATTAATAATCAGAAATTTAATAATGATA 779  
 QY 876 CCGAGAGTATGAATCTGAAGTTTCTTCATTCCTTCAATTTCAATATGAAATTAACACA 935  
 Db 780 CCGAGAGTATGAATCTGAAGTTTCTTCATTCCTTCAATTTCAATATGAAATTAACACA 839  
 QY 936 TGTATTTTCAATATCAGAAATGAGCAGTTCATCTCACAGAGACTGACGCTGA 995  
 Db 840 TGTATTTTCAATATCAGAAATGAGCAGTTCATCTCACAGAGACTGACGCTGA 899  
 QY 996 AAGGTATAGGCTCTCCAAAATGAGAGTCCCTGTGTATCATTCACCTAATGATCAT 1055  
 Db 900 AAGGTATAGGCTCTCCAAAATGAGAGTCCCTGTGTATCATTCACCTAATGATCAT 959











Mon Dec 27 15:31:09 2004

us-08-917-710-1.rge

Page 11

methods Patent: US 6280955-A 1 28-AUG-2001,  
JOURNAL Location/Qualifiers  
FEATURES 1..1740  
SOURCE /organism="unknown"  
ORIGIN /mol\_type="unassigned DNA"

Query Match	49.0%;	Score 1056.8;	DB 6;	Length 1740;
Best Local Similarity	99.8%;	Pred. No. 4.4e-210;		
Matches 1058;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	294	TCTCAAGAGATGACACCTCTGGGTGTATGAGTCTCTCACTTTATGAAATCCTGGCA	353
Db	1	TCTCAAGAGATGACACCTCTGGGTGTATGAGTCTCTCACTTTATGAAATCCTGGCA	60
QY	354	AGTATGCTTCAGAACGTGGGATGACTGGGGACTAGACACCATAGGCCAATCCAACTG	413
Db	61	AGTATGCTTCAGAACGTGGGATGACTGGGGACTAGACACCATAGGCCAATCCAACTG	120
QY	414	TTTGAAGATGAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTCTGAATTTCAAC	473
Db	121	TTTGAAGATGAGCCAGCTCGCATCAAGTGGCCACTCTTTGAACACTTTCTGAATTTCAAC	180
QY	474	TACAGCAGCCCATTCAGCTGAGCCTTACTGATCTGTATTTGGACTTAAGCAGGACCGG	533
Db	181	TACAGCAGCCCATTCAGCTGAGCCTTACTGATCTGTATTTGGACTTAAGCAGGACCGG	240
QY	534	GACCTGAGGAGCCCAATTAATCTCCGCGCTCCCGGAAACCGCATTAAGTAAGGAGAAACAT	593
Db	241	GACCTGAGGAGCCCAATTAATCTCCGCGCTCCCGGAAACCGCATTAAGTAAGGAGAAACAT	300
QY	594	GTGCTGTGGTTCCGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGCACTTTAAG	653
Db	301	GTGCTGTGGTTCCGGCCCACTCTCTCTCAATGACACTGGCAACTATACCTGCACTTTAAG	360
QY	654	AACACTACATATTTGGACGAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAGAACAAGCTGT	713
Db	361	AACACTACATATTTGGACGAAGTTGCATTTCCCTTGGAAAGTTGTTCAAAAGAACAAGCTGT	420
QY	714	TTCAATTTCCCATGAAATCCCACTGATGAATACGTATATAGAAATATGCAATTCAGAG	773
Db	421	TTCAATTTCCCATGAAATCCCACTGATGAATACGTATATAGAAATATGCAATTCAGAG	480
QY	774	ATCACTGTTCCAATATGATGATATTTTCCCTTCCAGTGTCAAAACCACTATCACTTGG	833
Db	481	ATCACTGTTCCAATATGATGATATTTTCCCTTCCAGTGTCAAAACCACTATCACTTGG	540
QY	834	TATATGAGCTGTATTAATAATACAGAAATTTTATATATGTAATACCCGAGAGTATGAACCTG	893
Db	541	TATATGAGCTGTATTAATAATACAGAAATTTTATATATGTAATACCCGAGAGTATGAACCTG	600
QY	894	AGTTTCTCATTTGCTTAAATTTCAAAATATGAAATTAACAATGTGTTTATCATATCCA	953
Db	601	AGTTTCTCATTTGCTTAAATTTCAAAATATGAAATTAACAATGTGTTTATCATATCCA	660
QY	954	GAAATGAGAGTAAGTTTCATCTCCAGAGACTCGATGTAAAGTATGAGGCTCTCCA	1013
Db	661	GAAATGAGAGTAAGTTTCATCTCCAGAGACTCGATGTAAAGTATGAGGCTCTCCA	720
QY	1014	AAAAATGACAGTCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATAGAAAGAA	1073
Db	721	AAAAATGACAGTCCCCCTGTGATCCATTCACCTAATGATCATGTGTCTATAGAAAGAA	780
QY	1074	CCAGAGAGAGCTACCTCATTTCCCTGTACGGCTTATTAAGTTTCGATAGATCTCTGC	1133
Db	781	CCAGAGAGAGCTACCTCATTTCCCTGTACGGCTTATTAAGTTTCGATAGATCTCTGC	840
QY	1134	AATGAGGTTTGGTGAGCACTTGATGAAAAAAACCTGTATGACATCACTATTTGATCTCAC	1193
Db	841	AATGAGGTTTGGTGAGCACTTGATGAAAAAAACCTGTATGACATCACTATTTGATCTCAC	900
QY	1194	ATTAAACGAAAGTATAGTCAATGTATGAAACAGAAAGTAAACCTAGAACTCAAGTTTGAAG	1255

Db 901 ATTATCGAAGTATTAAGTCATAGTAGAACAAGAGATGAACAAGAACTCAGATTTTGAGC 960

Qy 1354 ATCAAGAAAGTACCTCTGAGATCTCAACGCGCATATGCTGTCACTGCTAGAGAGGCC 1313

Db 961 ATCAAGAAAGTACCTCTGAGGATCTCAAGCGCAGCTATGCTGTCACTGAGAGAGGCC 1020

Qy 1314 AAAGCGAAGTGGCAAGCAGCCAGGTGAGCAGAGAAG 1353

Db 1021 AAAGCGAAGTGGCAAGCAGCCAGGTGAGCAGAGAAG 1060

RESULT 10  
AF029213  
LOCUS AF029213 1740 bp mRNA linear PRI 30-SEP-1999  
DEFINITION Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.  
ACCESSION AF029213  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 1740)  
TITLE Huang, J., Gao, X., Li, S. and Cao, Z.  
JOURNAL Recruitment of IRAK to the interleukin 1 receptor complex requires  
Interleukin 1 receptor accessory protein (1997)  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)  
PUBMED 98058729  
9371760  
2 (bases 1 to 1740)  
Huang, J., Gao, X., Li, S. and Cao, Z.  
REFERENCE Direct Submission  
AUTHORS  
TITLE Submitted (07-OCT-1997) Biology, Tularek, Inc., 2 Corporate Dr.,  
JOURNAL South San Francisco, CA 94080, USA

```

FEATURES
Source
Location/Qualifiers
1..1740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="placenta"
10..1722
/codon_start=1
/product="IL-1 receptor accessory protein"
/protein_id="AA84059.1"
/db_xref="GI:2599127"
/translation="MTLLMCVSLHYEGILQSDASERCDMDGTNRKQICVFEEDEPAR
IKCGFEPHLPKENVSTASHAGLILVYWTRODRLEPINFRLLENKISKEQVLMFR
PTLLNDNGTQCLIRNTYTSKVAFLPENVOKSCFSPKGLIENKGIQDRICTG
PNDGPPRSVSKPIITWYMGCVKQIONNNVIPSQMI.SPIALI.SNNKNTCVATYEE
NGRTHLHTRLLTKRVYSS.PCAKADPVIHSNDHRYKREGEELLICTYAFSLMS
RNEWMAITDKKPDIDITDVTINBSHSHSTEDETRQIILSIKATYSEDLKRSYVCH
RSKAGEYAKARKQKQPARVYVELCGFGATVAVVLIIVTHVYVLEWLVRYAH
FGDDETILIDKEVDIIVLSPNYALQOGLLELKAQGLNNASRGNIINIVLYQVAYKE
TDELPSIQKSRRLIVLSPNYALQOGLLELKAQGLNNASRGNIINIVLYQVAYKE
TKYVELTKRAKTIVLTIVKMKGEKSKYPOGRFWKQLOVAMPYKKSRRSSSDQGLSYSS
LKQIV"
ORIGIN
Query Match 49.0%; Score 1056.8; DR 9; Length 1740;
Best Local Similarity 99.8%; Pred. No. 4.4e-210;
Matches 1058; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Oy	294	TCTCAAGAGATGACCTTCTGTGTGTGTGTGTGTGTGTCTCTACTTTTATGTAAATCCTGCAA	353
Db	1	TCTCAAGAGATGACCTTCTGTGTGTGTGTGTGTGTGTCTCTACTTTTATGTAAATCCTGCAA	60
Oy	354	AGTATGCTCCATGAAACGCTGTGAGATGCTGGGGAATTAGACACATGAGCAAAATCCAAAGTG	413
Db	61	AGTATGCTCCATGAAACGCTGTGAGATGCTGGGGAATTAGACACATGAGCAAAATCCAAAGTG	120
Oy	414	TTTGAATATAGCCAGATGCAATGAATGCGCACTCTTTGAACACTTCTTGAATTCAC	473



QY 1143 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTGACCATTAAAGAA 1202  
DB 841 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTGACCATTAAAGAA 900  
QY 1203 AGTAAATCTGATGATGAGAACAGAAAGATGAAATCTGAAATCTGAAATCTGAAATCTGAA 1262  
DB 901 AGTAAATCTGATGATGAGAACAGAAAGATGAAATCTGAAATCTGAAATCTGAAATCTGAA 960  
QY 1263 GTTACCTCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1322  
DB 961 GTTACCTCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1020  
QY 1323 GTTGCCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1353  
DB 1021 GTTGCCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1051

RESULT 12  
AX704564 2064 bp DNA linear PAT 03-APR-2003  
LOCUS DEFINITION Sequence 1 from Patent WO02064630.  
AX704564  
ACCESSION AX704564  
VERSION AX704564.1 GI:29538642  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1  
AUTHORS Sims, J.E. and Smith, D.E.  
TITLE IL-1 receptor accessory protein  
JOURNAL Patent: WO 02064630-A-1 22-AUG-2002;  
IMMUNEX CORPORATION (US)  
FEATURES  
source location/Qualifiers  
1..2064  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
1..2064  
/note="unassigned protein product"  
/codon\_start=1  
/protein\_id="CAD87724.1"  
/db\_xref="GI:29538643"  
/translation="MTLMCVSLVYFGILQSDASERCDMDLDMRQIOVFEPBPAP  
IKCLPHEFKENYSTASHAGLTLTWVTRDRLDLEPILPENTISKEKDLMPR  
PTLNDNTNYTOMLBNNTYCGKVAFLPVLVQKDCSPMLPVRKLIYRIGTORITC  
FNVDGYPSSVAPKPTITWVTCYKIQENNVNIPKGNVLSFLALISNNAGTCVATYE  
NGRPFHLTRLLTVKVGSPKNAFVPIVISHPNDAVYKEPEBELIICTVFSLIMS  
RNEVWTTIDGKKPDITIDVTINESISHSTEDERTDILSIKVTEDELRSYVCA  
RSAGEVAKAKKOKVAPRYVLAAGFATVLLVYLIVVHYVLEWLYRYAH  
FGDETLIDGKEVDIVSARNAEHEEVEVLLTGLVLENERGYLCIFDRSLPGNT  
VBAYVDFIQSRBNMIVISPDYVTEKLSMLPFLGVWCONSIAIKLIVYEREP  
HPGILQLESVSVSWKEKSKHSKSKLRLALPLRSLSAGSNNESCSGSDIS  
LDHVGRRSRLEKPEPELOSSERAAGSPAPGSMKHKRSKSAATCRCCVTCGSHLR  
NKSRAEIHNOQWETHLCKPVPOSETWIONGTRELPAPQISALALHHTDLSNN  
DEVIL"

misc\_feature  
1792  
/note="n = a or c. Xaa at amino acid position 598 is Thr  
or Pro."

ORIGIN  
Query Match 48.6%; Score 1047.8; DB 6; Length 2064;  
Best Local Similarity 99.8%; Pred. No. 3.4e-208;  
Matches 1049; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 423 GAGCCAGCTGCGATCAAGTGGCCACTCTTTGAAACCTTCTTGAAATCTCACTACAGACA 482  
DB 121 GAGCCAGCTGCGATCAAGTGGCCACTCTTTGAAACCTTCTTGAAATCTCACTACAGACA 180  
QY 483 GCCCATTCGCTGGCCCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 542  
DB 181 GCCCATTCGCTGGCCCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240  
QY 543 GAGCCATTAATCTTCGCTCCCGGAAACCGCATTAAGTAAAGAAAGATGTCTGTGG 602  
DB 241 GAGCCATTAATCTTCGCTCCCGGAAACCGCATTAAGTAAAGAAAGATGTCTGTGG 300  
QY 603 TTCCGGCCCACTCTCTCAATGACACTGGCACTAATACCTGATCTGATCTGATCTGATCTG 662  
DB 301 TTCCGGCCCACTCTCTCAATGACACTGGCACTAATACCTGATCTGATCTGATCTGATCTG 360  
QY 663 TATTGACGAAAGTTCATTTCCCTGGAAGTGTCAAAAAGACAGCTGTTCAATTCC 722  
DB 361 TATTGACGAAAGTTCATTTCCCTGGAAGTGTCAAAAAGACAGCTGTTCAATTCC 420  
QY 723 CCATGAACTCCCATGCTAATGATGATGATGATGATGATGATGATGATGATGATGATG 782  
DB 421 CCATGAACTCCCATGCTAATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
QY 783 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842  
DB 481 CCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
QY 843 TGTATTAATTAATGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 902  
DB 541 TGTATTAATTAATGAAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600  
QY 903 ATTGCTTAATTTCAAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATG 962  
DB 601 ATTGCTTAATTTCAAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATG 660  
QY 963 CGTACGTTTCACTCAACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1022  
DB 661 CGTACGTTTCACTCAACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 720  
QY 1023 GTGCCCCCTGTGATCCATTTCACTTAATGATGATGATGATGATGATGATGATGATGATG 1082  
DB 721 GTGCCCCCTGTGATCCATTTCACTTAATGATGATGATGATGATGATGATGATGATGATG 780  
QY 1083 GAGCTACTATCCCTGAGACGGCTATTTAGTTCTGATGATGATGATGATGATGATGATGATG 1142  
DB 781 GAGCTACTATCCCTGAGACGGCTATTTAGTTCTGATGATGATGATGATGATGATGATGATG 840  
QY 1143 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTGACCATTAAAG 1202  
DB 841 TGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTGACCATTAAAG 900  
QY 1203 AGTAAATCTGATGATGAGAACAGAAAGATGAAATCTGAAATCTGAAATCTGAAATCTGAA 1262  
DB 901 AGTAAATCTGATGATGAGAACAGAAAGATGAAATCTGAAATCTGAAATCTGAAATCTGAA 960  
QY 1263 GTTACCTCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1322  
DB 961 GTTACCTCTGAGGATCTCAAGGAGCAGTATGCTGTCTGATGATGATGATGATGATGATG 1020

RESULT 13  
BD231181 2733 bp DNA linear PAT 17-JUL-2003  
LOCUS DEFINITION Antagonist based on receptor and preparation and utilization  
ACCESSION BD231181  
VERSION BD231181.1 GI:33040951

KEYWORDS	JP 2002525119-A/7.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	Stahl,N. and Yancopoulos,G.D.
JOURNAL	Antagonist based on receptor and prepration and utilization methods Parent: JP 2002525119-A 7 13-AUG-2002; REGENERON PHARMACEUTICALS INC
COMMENT	OS Homo sapiens (human) PN JP 2002525119-A/7 PD 13-AUG-2002 PF 22-SEP-1999 JP 2000572379 PI 25-SEP-1998 US 60/101858.19-MAY-1999 US 09/313942 PI NELI STAHL,GEORGE D YANCOPOULOS PC C12N15/09,C07K41/715,C07K19/00,C12M1/19,C12N1/21,C12N5/10, PC C12P21/02// PC A61K38/00,A61P19/10,A61P35/00,(C12P21/02,C12R1:91),C12N15/00, PC C12N5/00, PC A61K37/02 CC Antagonist based on receptor and prepration and utilization CC FH Key FI CDS Location/Qualifiers (1)..(2730).
FEATURES	source Location/Qualifiers . .2733 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
ORIGIN	
Query Match	48.4%; Score 1043; DB 6; Length 2733;
Best Local Similarity	99.5%; Pred.No. 3.4e-207;
Matches 1046; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	303 ATGACACTTCTGTGTGTGTAGTCCTCACTTTATGGAATCGGCAGAATGCC 362
Db	1 ATGGTGCTTCTGTGTGTGTAGTAGTCCTCACTTTATGGAATCTGCAAAGTGAAGCC 60
QY	363 TCAGAACCTCCAGATGACCTGGGAGCATAGACAACATGAGCAAATCCAAGTTTGAAGAT 422
Db	61 TCAAGACCTTCGATGACTGGGGATACACACATGAGCAAATCCAAGTTTGAAGAT 120
QY	423 GAGCCAGCTGCATCAAGTGCCCACTCTTGAACACTTCTGAAATTCACTACACACA 482
Db	121 GAGCCAGCTCCCACTCAAGTGCCCACTCTTGAACACTTCTGAAATTCACTACAGCACCA 180
QY	483 GCCAATTCAGTGGGCTTAAGTCTGATCGTATGGAATGACATAAGCAAGGACCGGACCTTGAG 542
Db	181 GCCAATTCAGTGGGCTTAAGTCTGATCTGATCTGATGGAATGACATAAGCAAGGACCGGACCTTGAG 240
QY	543 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAGAGAAAAGATGTGCTGGG 602
Db	241 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAGAGAAAAGATGTGCTGGG 300
QY	603 TTCCGGGCCCAATCCCTCCATAGACACGCGGACATTAACCTGATGTTAAGAAACATACA 662
Db	301 TTCCGGGCCCAATCCCTCCATAGACACGCGGACATTAACCTGATGTTAAGAAACATACA 360
QY	663 TAATGACAGCAAGTTGCAATTCCTCTGGAAATTGTTCAAAAAAGACAGCTGTTCAATTC 722
Db	361 TAATGACAGCAAGTTGCAATTCCTCTGGAAATTGTTCAAAAAAGACAGCTGTTCAATTC 420
QY	723 CCCATGAATCTCCAGTGCAATAACTGTATATAGATATGGAATTCAGAGATCACTTGT 782
Db	421 CCCATGAATCTCCAGTGCAATAACTGTATATAGATATGGAATTCAGAGATCACTTGT 480
QY	783 CCAATATGATGATATTTTCCTCCAGTCAAAACGCAATATCACTGGTATATGAGC 842
Db	481 CCAATATGATGATATTTTCCTCCAGTCAAAACGCAATATCACTGGTATATGAGC 540
QY	843 TGTTATAAATATACGAATTTTAAATATGTAATACCAGAGATATGAACCTTGATTTCTC 902

Db	541	TGTTATATAAAATACAGAAATTTTAATTAAGTATATACCCGAGAGTATGAACCTTAGTTCTCTC	600
QY	903	ATTGCTTAATTTCAAATATGAAATTTACACATGTGTTGTTACATATCCGAAATAATGGA	962
Db	601	ATTGCTTAATTTCAAATATGAAATTTACACATGTGTTGTTACATATCCGAAATAATGGA	660
QY	963	CGTAGGTTTCACTCAACAGACCTCTGACGTAAAGGATGAGTCTCCCAAAAATATGCA	10222
Db	661	CGTAGGTTTCACTCAACAGACCTCTGACGTAAAGGATGAGTCTCCCAAAAATATGCA	720
QY	1023	GTGCCCCCTGTGATTCATTCACCTTAATGATCATGTGTCTATGAGAAAGAACCGAGAGAG	10822
Db	721	GTGCCCCCTGTGATTCATTCACCTTAATGATCATGTGTCTATGAGAAAGAACCGAGAGAG	780
QY	1083	GAGCTACTCATCTCCCTGTAGAGGCTGATTTTATAGTTTCTGTAGATGATTCCTCCGAATGAGATT	11422
Db	781	GAGCTACTCATCTCCCTGTAGAGGCTGATTTTATAGTTTCTGTAGATGATTCCTCCGAATGAGATT	840
QY	1143	TGCTGGAACCAATTGATGGAAGAAAAAAACCTGATGACATCACTATTGATGTCAACATTAAACGA	12022
Db	841	TGCTGGAACCAATTGATGGAAGAAAAAAACCTGATGACATCACTATTGATGTCAACATTAAACGA	900
QY	1203	AGTAAAGTCACTACTATATAACAGAAATGAAAGCTAGAACTAGATTTTGAAGATCAAGAA	12622
Db	901	AGTAAAGTCACTACTATATAACAGAAATGAAAGCTAGAACTAGATTTTGAAGATCAAGAA	960
QY	1263	GTTACTCTGTGAGACTCAAGCCAGCTATGTCTGTATGCTAGTAAGTGCACAAAGCGAA	13222
Db	961	GTTACTCTGTGAGACTCAAGCCAGCTATGTCTGTATGCTAGTAAGTGCACAAAGCGAA	1020
QY	1323	GTTGCCAAGACGACCAAGGTGAGACAGAAAG	1353
Db	1021	GTTGCCAAGACGACCAAGGTGAGACAGAAAG	1051

RESULT 14

CQ796431

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

source

CDS

1

Stahl, N. and Yancopoulos, G.D.

Il-4 trap based on IL receptor fusion proteins

Patent: EP 1405915-A 27 07-APR-2004;

REGENERON PHARMACEUTICALS, INC. (US)

Location/Qualifiers

1..2733

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

1..2733

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAG26525.1"

/db\_xref="GI:46408205"

/translation="MTLLMCFVSLIYFYGILOSASERCDMDGLTMRQIVPEDEPAR

IKCPLEPHLKENVSTAHSAAGLILIMTRRODLEPIRFLPBNRISKEKVLMR

PIRLNDGPHLCMLRNTTYSKAPLEAVYQKSCRNPSPKVLVYKLTIEYGIORIC

PNDVGFPSVSVKFLITWYMGCAKIQNNVITPRGMDLFLIALISNGATTCVYTPE

NGSTFHLTRLTVKVVGPSKNAPVPVISHENDHVVYKEGEBELLPCVYFSFLMDS

RNFWMMITIDKSPDDITIDVTINESISHSTDEBETROIISIKVTSBDAKRSYVCHA

RSKAGKEAAKAKYKQKVPARYVSGAPMLSEADKKEBEKILIVSANEIDVPC

PLNDEHKGTITWKDSKTPVTEGQSRILHOKEXKLMPVAKVEDSGHYCVVRNS

YCRILTSKQVNEPMLCYNAQAITPKQLPVAGDGLVQVPMFKNENNELPKIQW

YKCKPILLDNTHFSQYKRLIYMNATBEKRGNYTCHASTYTIKQYPIRIVPEPTL

ENKPKRPVIVSPANETMEVDLSQQLICNVTVGLSDLAIVYKMSGVIDEEDVPVGE





```
Db      541 TGTATATAAATACAGAAATTTTAATATATGTAATACCCGAGGTATGAATTGATTCCTC 600
Qy      903 ATTGCTTAATTTCAATATATGAAATTTACACATGTGTTTACATATCCAGAAAATGA 962
Db      601 ATTGCTTAATTTCAATATATGAAATTTACACATGTGTTTACATATCCAGAAAATGA 660
Qy      963 CGTACGTTTCATCTCCAGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 1022
Db      661 CGTACGTTTCATCTCCAGAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA 720
Qy      1023 GTGCCCCCTGTGATGCATTCACCTATATGATCATGTGATCTATGAGAAAAGAACAGAGAG 1082
Db      721 GTGCCCCCTGTGATGCATTCACCTATATGATCATGTGATCTATGAGAAAAGAACAGAGAG 780
Qy      1083 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGATTTCTGCAATGAGGT 1142
Db      781 GAGCTACTCATTCCTGTACGGTCTATTTAGTTTCTGATGATTTCTGCAATGAGGT 840
Qy      1143 TGGTGGACCATTTGATGAGAAAAAAACCTGATGATCATCTATTGATGTCACCATTAAGCA 1202
Db      841 TGGTGGACCATTTGATGAGAAAAAAACCTGATGATCATCTATTGATGTCACCATTAAGCA 900
Qy      1203 AGTATAAGTCATATAGTAGAACAAGAGATGAAACTAGAACTCAGATTTTGGCATCAAGAAA 1262
Db      901 AGTATAAGTCATATAGTAGAACAAGAGATGAAACTAGAACTCAGATTTTGGCATCAAGAAA 960
Qy      1263 GTTACCTCTGAGGATCTCAAGGCGAGCTATGTCTGTCAATGCTAGAAAGTCCAAAGCGGA 1322
Db      961 GTTACCTCTGAGGATCTCAAGGCGAGCTATGTCTGTCAATGCTAGAAAGTCCAAAGCGGA 1020
Qy      1323 GTTGCCAAAGCAGCCAGGTGAGCAGAAAAG 1353
Db      1021 GTTGCCAAAGCAGCCAGGTGAGCAGAAAAG 1051
```

Search completed: December 25, 2004, 17:40:30  
Job time : 3066 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:53:49 ; Search time 1036 Seconds

(without alignments)  
10919.404 Million cell updates/secTitle: US-08-917-710-1  
Perfect score: 2155  
Sequence: 1 CGGTCGGCGCCGCTCTAGAA.....CTAAAAAAAAAAAAAAAAAAAA 2155Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*\n1: Geneseqn1980s:\*\n2: Geneseqn1990s:\*\n3: Geneseqn2000s:\*\n4: Geneseqn2001as:\*\n5: Geneseqn2001bs:\*\n6: Geneseqn2002as:\*\n7: Geneseqn2002bs:\*\n8: Geneseqn2003as:\*\n9: Geneseqn2003bs:\*\n10: Geneseqn2003cs:\*\n11: Geneseqn2003ds:\*\n12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	98.4	2155	2	AAV23659 Human int
2	2017.6	93.6	2035	10	ADF90863 Human hep
3	1242.8	57.7	4724	10	AAD51467 IL-1 rece
4	1242.8	57.7	4724	12	ADP13278 Renal cel
5	1056.8	49.0	1740	5	AA815608 Human int
6	1047.8	48.6	1713	8	ABX12962 DNA encod
7	1047.8	48.5	2064	6	ABQ81182 Human IL-
8	1046.2	48.5	1077	2	AA732027 Soluble i
9	1046.2	48.5	1077	2	ACC48599 Soluble i
10	1046.2	48.5	1713	9	AA732026 Human int
11	1046.2	48.5	1713	9	ACC48598 Human int
12	1043	48.4	2703	10	AA683748 Human IL-
13	1043	48.4	2709	10	AA683750 Human IL-
14	1043	48.4	2709	10	AA683772 Human IL-
15	1043	48.4	2709	10	AA683749 Human IL-
16	1043	48.4	2715	10	AA683774 Human IL-
17	1043	48.4	2715	10	AA683773 Human IL-
18	1043	48.4	2733	3	AA09048 Fusion po
19	1043	48.4	2738	10	AA683742 Human cyt
20	1043	48.4	2748	10	AA683754 Human IL-
21	1043	48.4	2754	10	AA683755 Human IL-

22	1043	48.4	2754	10	AA683756 Human IL-
23	1043	48.4	2754	10	AA683778 Human IL-
24	1043	48.4	2754	10	AA683779 Human IL-
25	1043	48.4	2760	10	AA683780 Human IL-
26	1041.4	48.3	2703	10	AA683760 Human IL-
27	1041.4	48.3	2709	10	AA683761 Human IL-
28	1041.4	48.3	2709	10	AA683762 Human IL-
29	1041.4	48.3	2748	10	AA683766 Human IL-
30	1041.4	48.3	2754	10	AA683767 Human IL-
31	1041.4	48.3	2754	10	AA683768 Human IL-
32	988.8	45.9	2748	10	AA683751 Human IL-
33	988.8	45.9	2754	10	AA683753 Human IL-
34	988.8	45.9	2754	10	AA683752 Human IL-
35	987.8	45.8	2703	10	AA683745 Human IL-
36	987.8	45.8	2709	10	AA683769 Human IL-
37	987.8	45.8	2709	10	AA683746 Human IL-
38	987.8	45.8	2709	10	AA683747 Human IL-
39	987.8	45.8	2715	10	AA683770 Human IL-
40	987.8	45.8	2715	10	AA683771 Human IL-
41	987.8	45.8	2754	10	AA683775 Human IL-
42	987.8	45.8	2760	10	AA683776 Human IL-
43	987.8	45.8	2760	10	AA683777 Human IL-
44	987.2	45.8	2748	10	AA683763 Human IL-
45	987.2	45.8	2754	10	AA683765 Human IL-

## ALIGNMENTS

RESULT 1  
ID AAV23659 standard, cDNA, 2155 BP.  
AC AAV23659;  
DT 17-AUG-1998 (first entry)  
XX Human interleukin-1 receptor accessory molecule cDNA.  
DE Human interleukin-1 receptor accessory molecule cDNA.  
XX Interleukin-1 receptor accessory molecule; IL-1R ACW; human;  
KM signal transduction; infection; septic shock; inflammation;  
KM rheumatoid arthritis; therapy; ds.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 303..1373 /\*tag= a  
FT sig\_peptide 303..353 /\*tag= b  
FT mat\_peptide 354..1370 /\*tag= c  
XX WC9808969-A1.  
XX 05-MAR-1998.  
XX 26-AUG-1996; 96MO-US013954.  
XX 26-AUG-1996; 96MO-US013954.  
XX 26-AUG-1996; 96MO-US013954.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Bednarik DP, Olsen HS, Rosen CA;  
XX WPL; 1998-230267/20.  
XX P-PSDB; AAWS3897.  
XX Nucleic acid encoding interleukin-1 receptor accessory protein - used for  
XX therapeutic modulation of IL-1 activity.  
XX Claim 2; Fig 1; 95BP; English.

This cDNA clone codes for human interleukin-1 receptor accessory molecule (IL1-R AcM) (see AF53897), a new member of the immunoglobulin superfamily that forms a complex with type 1 IL1-R and which has higher affinity for IL-1 than the receptor itself, suggesting that the known high and low affinity forms of IL1-R are in fact the receptor with or without IL1-R AcM, respectively. The 2155 bp sequence is present in clone HME352 (deposited as AF53897) derived from microvascular epithelium (no details of isolation given). Recombinant expression in *Escherichia coli*, mammalian and insect cells is described. Recombinant host cells and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see AF53898-915) of IL1-R AcM. Recombinant IL1-R AcM can be used to identify IL-1R agonists and antagonists useful for therapeutic modulation of IL-1 activity, and to raise specific antibodies. Nucleic acid fragments are useful as diagnostic probes and primers, for isolation of IL1-R AcM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that might be linked to disease

Sequence 2155 BP; 709 A; 429 C; 433 G; 584 T; 0 U; 0 Other;

Query Match 98.4%; Score 2120; DB 2; Length 2155;  
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 3; Gaps 3;  
Matches 2153; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

1 CGGTGGCGCCGCTTCTAGAACTAGTATGCCCGGAGTGCAGAAATTCGACAGAGAA 60  
1 CGGTGGCGCCGCTTCTAGAACTAGTATGCCCGGAGTGCAGAAATTCGACAGAGAA 60  
61 GTGCGCGGGAAGTAAAGGCTCACTGGGGAAGTCCGGGATCCAGTCTCCGGGCTC 120  
61 GTGCGCGGGAAGTAAAGGCTCACTGGGGAAGTCCGGGATCCAGTCTCCGGGCTC 120  
121 GCTTTGGCCAGAGGCGCGGAAAGAGAGTCCCGGAGTGCACACCAATCCCGGCTG 180  
121 GCTTTGGCCAGAGGCGCGGAAAGAGAGTCCCGGAGTGCACACCAATCCCGGCTG 180  
122 CGCTTTGGCCAGAGGCGCGGAAAGAGAGTCCCGGAGTGCACACCAATCCCGGCTG 180  
122 CGCTTTGGCCAGAGGCGCGGAAAGAGAGTCCCGGAGTGCACACCAATCCCGGCTG 180  
181 CTTTGTGCGCGCTCTCTAGTCTCCAAAGAAAGCATGTGATCATCATCTTAA 240  
181 CTTTGTGCGCGCTCTCTAGTCTCCAAAGAAAGCATGTGATCATCATCTTAA 240  
181 CTTTGTGCGCGCTCTCTAGTCTCCAAAGAAAGCATGTGATCATCATCTTAA 240  
241 ACTAAGATGAGAGGCGCTTAAAGGCTCACTTGGCCCTCTTAAATCTCTAAA 300  
241 ACTAAGATGAGAGGCGCTTAAAGGCTCACTTGGCCCTCTTAAATCTCTAAA 300  
241 ACTAAGATGAGAGGCGCTTAAAGGCTCACTTGGCCCTCTTAAATCTCTAAA 300  
241 ACTAAGATGAGAGGCGCTTAAAGGCTCACTTGGCCCTCTTAAATCTCTAAA 300  
301 GGATGACACTTCTGT 360  
301 GGATGACACTTCTGT 360  
301 GGATGACACTTCTGT 360  
301 GGATGACACTTCTGT 360  
361 CCTGGAAGCGTGCATGATGAGGAGCTAGACACCATAGGCAAAATCCAGTGTGAG 420  
361 CCTGGAAGCGTGCATGATGAGGAGCTAGACACCATAGGCAAAATCCAGTGTGAG 420  
361 CCTGGAAGCGTGCATGATGAGGAGCTAGACACCATAGGCAAAATCCAGTGTGAG 420  
361 CCTGGAAGCGTGCATGATGAGGAGCTAGACACCATAGGCAAAATCCAGTGTGAG 420  
421 ATGAGCCAGCTGCATCAAGTCCCACTCTTGAACACTTCTTGAATCAACTACACA 480  
421 ATGAGCCAGCTGCATCAAGTCCCACTCTTGAACACTTCTTGAATCAACTACACA 480  
421 ATGAGCCAGCTGCATCAAGTCCCACTCTTGAACACTTCTTGAATCAACTACACA 480  
421 ATGAGCCAGCTGCATCAAGTCCCACTCTTGAACACTTCTTGAATCAACTACACA 480  
481 CAGCCCATTCAGCTGGCTTACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
481 CAGCCCATTCAGCTGGCTTACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
481 CAGCCCATTCAGCTGGCTTACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
481 CAGCCCATTCAGCTGGCTTACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
481 CAGCCCATTCAGCTGGCTTACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
541 AGAGCCCAATTAATTCGCGCTCCCGGAGAACCGCATTAAGTAAAGAAATGTGTGT 600  
541 AGAGCCCAATTAATTCGCGCTCCCGGAGAACCGCATTAAGTAAAGAAATGTGTGT 600  
541 AGAGCCCAATTAATTCGCGCTCCCGGAGAACCGCATTAAGTAAAGAAATGTGTGT 600  
541 AGAGCCCAATTAATTCGCGCTCCCGGAGAACCGCATTAAGTAAAGAAATGTGTGT 600  
541 AGAGCCCAATTAATTCGCGCTCCCGGAGAACCGCATTAAGTAAAGAAATGTGTGT 600  
601 GGTTCCGCGCCACTCTCCCTCATATGACATGGGCACTATACCTGCTTAAGAACTA 660  
601 GGTTCCGCGCCACTCTCCCTCATATGACATGGGCACTATACCTGCTTAAGAACTA 660  
601 GGTTCCGCGCCACTCTCCCTCATATGACATGGGCACTATACCTGCTTAAGAACTA 660  
601 GGTTCCGCGCCACTCTCCCTCATATGACATGGGCACTATACCTGCTTAAGAACTA 660  
601 GGTTCCGCGCCACTCTCCCTCATATGACATGGGCACTATACCTGCTTAAGAACTA 660  
661 CATATTGAGCAAAATGTGATTTCCCTTGAAGTGTTCACAAAGACGCTGTTCATTT 720  
661 CATATTGAGCAAAATGTGATTTCCCTTGAAGTGTTCACAAAGACGCTGTTCATTT 720

721 CCCCATGAACTCCAGTGCATTAACCTATATAGAAATGGCATTCAGAGATCACTT 780  
721 CCCCATGAACTCCAGTGCATTAACCTATATAGAAATGGCATTCAGAGATCACTT 780  
721 CCCCATGAACTCCAGTGCATTAACCTATATAGAAATGGCATTCAGAGATCACTT 780  
781 GTCCAAATGATGATGATATTTTCTCCAGTGTCAACCGCATTCATCTGTGTATGG 840  
781 GTCCAAATGATGATGATATTTTCTCCAGTGTCAACCGCATTCATCTGTGTATGG 840  
781 GTCCAAATGATGATGATATTTTCTCCAGTGTCAACCGCATTCATCTGTGTATGG 840  
841 GCTGTTATTAATATGAAATTTTAAATATGATATATCCGAGGTATGAACCTGATTC 900  
841 GCTGTTATTAATATGAAATTTTAAATATGATATATCCGAGGTATGAACCTGATTC 900  
841 GCTGTTATTAATATGAAATTTTAAATATGATATATCCGAGGTATGAACCTGATTC 900  
841 GCTGTTATTAATATGAAATTTTAAATATGATATATCCGAGGTATGAACCTGATTC 900  
901 TCATTCCTTAATTTCAATTAATGAAATTAACATGATGTGTCTCATATCCAGAAATG 960  
901 TCATTCCTTAATTTCAATTAATGAAATTAACATGATGTGTCTCATATCCAGAAATG 960  
901 TCATTCCTTAATTTCAATTAATGAAATTAACATGATGTGTCTCATATCCAGAAATG 960  
901 TCATTCCTTAATTTCAATTAATGAAATTAACATGATGTGTCTCATATCCAGAAATG 960  
961 GAGTACGTTTATCTCAACAGAGCTCTGACCTGATGAAAGTATGAGCTCTCCAAATATG 1020  
961 GAGTACGTTTATCTCAACAGAGCTCTGACCTGATGAAAGTATGAGCTCTCCAAATATG 1020  
961 GAGTACGTTTATCTCAACAGAGCTCTGACCTGATGAAAGTATGAGCTCTCCAAATATG 1020  
961 GAGTACGTTTATCTCAACAGAGCTCTGACCTGATGAAAGTATGAGCTCTCCAAATATG 1020  
1021 CAGTCCCGCTGTGATCATTCACCTATGATCATGTGTCTATGAGAAAGAACAGAG 1080  
1021 CAGTCCCGCTGTGATCATTCACCTATGATCATGTGTCTATGAGAAAGAACAGAG 1080  
1021 CAGTCCCGCTGTGATCATTCACCTATGATCATGTGTCTATGAGAAAGAACAGAG 1080  
1081 AGAGCTACTCATTCCTGTAGGCTATTTTATGATTTTCTGATGATTCGCAATGAG 1140  
1081 AGAGCTACTCATTCCTGTAGGCTATTTTATGATTTTCTGATGATTCGCAATGAG 1140  
1081 AGAGCTACTCATTCCTGTAGGCTATTTTATGATTTTCTGATGATTCGCAATGAG 1140  
1081 AGAGCTACTCATTCCTGTAGGCTATTTTATGATTTTCTGATGATTCGCAATGAG 1140  
1141 TTGTGTGACACTTGTATGAGAAATTAACCTGATGATCATCTATGATGATCACTTAA 1200  
1141 TTGTGTGACACTTGTATGAGAAATTAACCTGATGATCATCTATGATGATCACTTAA 1200  
1201 AAAGTAAATGATATGATGAGAAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAA 1260  
1201 AAAGTAAATGATATGATGAGAAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAA 1260  
1201 AAAGTAAATGATATGATGAGAAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAA 1260  
1201 AAAGTAAATGATATGATGAGAAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAA 1260  
1261 AAGTACCTGTAGATCTCAAGGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320  
1261 AAGTACCTGTAGATCTCAAGGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320  
1261 AAGTACCTGTAGATCTCAAGGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320  
1261 AAGTACCTGTAGATCTCAAGGAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320  
1321 AAGTCCCAAGAGGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1380  
1321 AAGTCCCAAGAGGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1380  
1321 AAGTCCCAAGAGGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1380  
1321 AAGTCCCAAGAGGAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1380  
1381 CTGAGTCCCAATTAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
1381 CTGAGTCCCAATTAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
1381 CTGAGTCCCAATTAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
1381 CTGAGTCCCAATTAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
1381 CTGAGTCCCAATTAATTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
1441 GCTCCAGCACTAGCTGAGGAGTAAACCATATGATGATGATGATGATGATGATGAT 1500  
1441 GCTCCAGCACTAGCTGAGGAGTAAACCATATGATGATGATGATGATGATGATGAT 1500  
1441 GCTCCAGCACTAGCTGAGGAGTAAACCATATGATGATGATGATGATGATGATGAT 1500  
1441 GCTCCAGCACTAGCTGAGGAGTAAACCATATGATGATGATGATGATGATGATGAT 1500  
1501 ATATGAAAGTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1501 ATATGAAAGTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1501 ATATGAAAGTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1501 ATATGAAAGTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1561 GTATGCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
1561 GTATGCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
1561 GTATGCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
1561 GTATGCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
1561 GTATGCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620  
1621 TGTACAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAAT 1680  
1621 TGTACAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAAT 1680  
1621 TGTACAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAAT 1680  
1621 TGTACAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAAT 1680  
1621 TGTACAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAATTAATGAAAT 1680  
1681 ACTGTGAGGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1681 ACTGTGAGGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1681 ACTGTGAGGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1681 ACTGTGAGGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1681 ACTGTGAGGAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1741 AGAGTTTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
1741 AGAGTTTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
1741 AGAGTTTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
1741 AGAGTTTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
1741 AGAGTTTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800  
1801 TGAACAAATTAACGAAAGGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860  
1801 TGAACAAATTAACGAAAGGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860



QY 1242 CAGATTTGAGCATCAAGATTACCTCTGAGATCTCAGGCGAGTATGTCTCAT 1301  
 DB 1140 CAGATTTGAGCATCAAGATTACCTCTGAGATCTCAGGCGAGTATGTCTCAT 1139  
 QY 1302 GCTAGAGTGGCAAGGCGAAGTTGCCAAGACGCGAGTGAAGCAAGAAAGTATAGA 1361  
 DB 1200 GCTAGAGTGGCAAGGCGAAGTTGCCAAGACGCGAGTGAAGCAAGAAAGTATAGA 1259  
 QY 1362 TGGCGTCACTGATGATCTCTCAGTCCAAATTACATTTGGTGGATTAAGACAAAGG 1421  
 DB 1260 TGGCGTCACTGATGATCTCTCAGTCCAAATTACATTTGGTGGATTAAGACAAAGG 1319  
 QY 1422 AGAGATTAGAAACAAGAGAGCTCCAGACCTAGCCTGAGGCGATCTAACCATATGATG 1481  
 DB 1320 AGAGATTAGAAACAAGAGAGCTCCAGACCTAGCCTGAGGCGATCTAACCATATGATG 1379  
 QY 1482 AATCAACTTAAATGAAAAATATGAAAGTTTTCATCTATGTAAGTACTCAAAATATGTT 1541  
 DB 1380 AATCAACTTAAATGAAAAATATGAAAGTTTTCATCTATGTAAGTACTCAAAATATGTT 1439  
 QY 1542 TTCGATATTTGTTAGTACCGTATGCGCAATGTAGTAAATAATGAGCTGAGTACAG 1601  
 DB 1440 TTCGATATTTGTTAGTACCGTATGCGCAATGTAGTAAATAATGAGCTGAGTACAG 1499  
 QY 1602 TGAGACACAAATTTGTCTGTCTGACAAATTATGAAAAATTAAACAAAGAAATATTCAAA 1661  
 DB 1500 TGAGACACAAATTTGTCTGTCTGACAAATTATGAAAAATTAAACAAAGAAATATTCAAA 1559  
 QY 1662 GGTACCAAGATAGAAAAAAGTGTAGAGCCAAATGTGTGTAATTAATTAAGACCT 1721  
 DB 1560 GGTACCAAGATAGAAAAAAGTGTAGAGCCAAATGTGTGTAATTAATTAAGACCT 1619  
 QY 1722 TTTAAAAATCAATTCATGCTAGAGTTTAAGAGTCAATAAAAAAGATTCATCTGACCTA 1781  
 DB 1620 TTTAAAAATCAATTCATGCTAGAGTTTAAGAGTCAATAAAAAAGATTCATCTGACCTA 1679  
 QY 1782 AGACTTTGGGAAATTTTCTCTGACAAATTAACAAAGAAAGGATTTATATCTTTAAATTT 1841  
 DB 1680 AGACTTTGGGAAATTTTCTCTGACAAATTAACAAAGAAAGGATTTATATCTTTAAATTT 1739  
 QY 1842 AATTAAGAGATATCTGATGTTGTTAAACATTTATTAATAGAGCATCCATTTGATAGCA 1901  
 DB 1740 AATTAAGAGATATCTGATGTTGTTAAACATTTATTAATAGAGCATCCATTTGATAGCA 1799  
 QY 1902 ACTAAATTAAGATTAATGTTTATTTTCCAAAAATGCAATTAATTAATTTTAAA 1961  
 DB 1800 ACTAAATTAAGATTAATGTTTATTTTCCAAAAATGCAATTAATTAATTTTAAA 1859  
 QY 1962 CACTATGATCAATTTTAAAGAGGTTTAAATTAATTAACAGAGACGCAATTTGTAATG 2021  
 DB 1860 CACTATGATCAATTTTAAAGAGGTTTAAATTAATTAACAGAGACGCAATTTGTAATG 1919  
 QY 2022 AAAATCATTTAAATATGATTTTAAATGTAATACATGATTTCTATGTAATGTA 2081  
 DB 1920 AAAATCATTTAAATATGATTTTAAATGTAATACATGATTTCTATGTAATGTA 1979  
 QY 2082 TTTTATTTCAATTAATGGAATTAATTAAGCTTTCTTGAGAGGCTGCTCT 2137  
 DB 1980 TTTTATTTCAATTAATGGAATTAATTAAGCTTTCTTGAGAGGCTGCTCT 2035

RESULT 3  
 AAD51467  
 ID AAD51467 standard; DNA; 4724 BP.  
 AC AAD51467;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE IL-1 receptor accessory protein (IL-1Rac) gene.  
 XX  
 KW Drug screening; fungicide; gene therapy; antibacterial; infection; IL-1;

KM virucide; Interleukin-1; IL-1 receptor accessory protein; IL-1Rac; gene;  
 KW de.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 207..1919  
 FT /tag= a  
 FT /product= "IL-1Rac protein"  
 PN  
 XX  
 PD W02002101015-A2.  
 PD 19-DEC-2002.  
 PF 11-JUN-2002; 2002W0-US018346.  
 PF 11-JUN-2001; 2001US-0297305P.  
 PR (INTE-) INTERLEUKIN GENETICS INC.  
 PA  
 XX  
 PI Power S, Duff GW;  
 DR WPI; 2003-148793/14.  
 DR P-PSDB; AAB33567.  
 XX  
 PT New detection reagent, useful for monitoring molecular assembly events to  
 PT permit the dissection of genetic and non-genetic influences on biological  
 PT activity, comprises an interactive sensor pair.  
 XX  
 PS Disclosure; Fig 9; 56pp; English.  
 XX  
 CC The invention relates to methods, compositions and apparatus for  
 CC monitoring molecular assembly events. It also relates to a detection  
 CC reagent comprising an interactive sensor pair. The detection reagent is  
 CC useful for monitoring molecular assembly events to permit the dissection  
 CC of genetic and non-genetic influences on a particular biological  
 CC activity. The method is useful for linking genetic variations to  
 CC molecular and physiological events, drug screening, diagnostics, therapy  
 CC selection and dosing, patient monitoring or environmental safety. The  
 CC interactive sensor pairs may be used to screen for and identify novel  
 CC agonists and antagonists or other molecules that modulate a biological  
 CC activity. The method is also useful for selecting an appropriate targeted  
 CC therapeutic for a subject having an infection, including viral, bacterial  
 CC or fungal infection. It is also used in gene therapy. The present  
 CC sequence is interleukin-1 receptor accessory protein (IL-1Rac) gene. This  
 CC sequence is used to illustrate the method of the invention  
 XX  
 SQ Sequence 4724 BP; 1422 A; 902 C; 902 G; 1498 T; 0 U; 0 Other;  
 XX  
 Query Match 57.7%; Score 1242.8; DB 10; Length 4724;  
 Best Local Similarity 99.8%; Pred. No. 1.3e-279;  
 Matches 1255; Conservative 0; Mismatches 2; Indels 1; Gaps 1;



QY	396	ATGAGGCAAAATCCAAAGGTTTGAAGATGAGCCAGCTCGATCAATAGTCCACTCTTTGAA	455
Dp	300	ATGAGGCAAAATCCAAAGGTTTGAAGATGAGCCAGCTCGATCAATAGTCCACTCTTTGAA	359
QY	456	CACCTCTTGAAGATTCATACAGCAAGCCCATTCAGTGGCTTACTGTGATCTGTAT	515
Dp	360	CACCTCTTGAAGATTCATACAGCAAGCCCATTCAGTGGCTTACTGTGATCTGTAT	419
QY	516	TGACTAAGCAGGACCGGGACCTTGAGAGGCCAATTAACCTCCGCTCCGGAGAACCG	575
Dp	420	TGACTAAGCAGGACCGGGACCTTGAGAGGCCAATTAACCTCCGCTCCGGAGAACCG	479
QY	576	ATTAGTAGAGGAAAGATGTGCTGTGGTTCCGGCCCACTCTCCATAGACACTGGCAAC	635
Dp	480	ATTAGTAGAGGAAAGATGTGCTGTGGTTCCGGCCCACTCTCCATAGACACTGGCAAC	539
QY	636	TATACCGCAGATGTAAAGAAACATAATATGACAGCAAGTGGATTTCCCTGGAGATT	695
Dp	540	TATACCGCAGATGTAAAGAAACATAATATGACAGCAAGTGGATTTCCCTGGAGATT	599
QY	696	GTTCAAAAAGACAGCTGTTTCATATCCCATGAAACTCCAGTGCATAAATCTATATA	755
Dp	600	GTTCAAAAAGACAGCTGTTTCATATCCCATGAAACTCCAGTGCATAAATCTATATA	659
QY	756	GAATATGGCATTCAGAGGATCACTGTCCAAATGTATGATATTTTCCCTCCAGTGC	815
Dp	660	GAATATGGCATTCAGAGGATCACTGTCCAAATGTATGATATTTTCCCTCCAGTGC	719
QY	816	AAACCGACATCACTGGTATAGGGCTGTATATAAAATACAGAAATTTAATATATATATA	875
Dp	720	AAACCGACATCACTGGTATAGGGCTGTATATAAAATACAGAAATTTAATATATATATA	779
QY	876	CCCGAAGGTATGAACTTGAGTTTCTCATTTGCTCTTAATTTCAATATGAAATATACA	935
Dp	780	CCCGAAGGTATGAACTTGAGTTTCTCATTTGCTCTTAATTTCAATATGAAATATACA	839
QY	936	TGTGTGTTCATATCCAGAAAAATGAGACTAGTTCATCCACAGAGCTCTAGCTATA	995
Dp	840	TGTGTGTTCATATCCAGAAAAATGAGACTAGTTCATCCACAGAGCTCTAGCTATA	899
QY	996	AAGGTATAGGCTCTCCAAAAATGCAAGTCCCTGTGATCATTCACCTAATGATCAT	105
Dp	900	AAGGTATAGGCTCTCCAAAAATGCAAGTCCCTGTGATCATTCACCTAATGATCAT	959
QY	1056	GTGGTCTATAGAAAGAACACAGAGAGAGCTACTCATCCCTGTAGCGGTATATTAGT	111
Dp	960	GTGGTCTATAGAAAGAACACAGAGAGAGCTACTCATCCCTGTAGCGGTATATTAGT	101
QY	1116	TTTCTGATGGATTTCTGCAATGAGGTTTGTGTGACCATGTATGAGAAAAAAACCTGATGAC	117
Dp	1020	TTTCTGATGGATTTCTGCAATGAGGTTTGTGTGACCATGTATGAGAAAAAAACCTGATGAC	107
QY	1176	ATCACTATTGATGTCCACCATTAACGAAGATATATATCATATATAGAACAGAAATGAAACT	123
Dp	1080	ATCACTATTGATGTCCACCATTAACGAAGATATATATCATATATAGAACAGAAATGAAACA	113
QY	1236	AGAACTCAGATTTTGAAGATCAAGAAAGTTAACCCTGTGAGATCTCAAGCGCAGTATGTC	129
Dp	1140	AGAACTCAGATTTTGAAGATCAAGAAAGTTAACCCTGTGAGATCTCAAGCGCAGTATGTC	119
QY	1296	TGTCAATGTCTGAAGTCCCAAGCGCAAGTTGGCCAAAGACGCCAAGGTGAGACGAGAAAG	1353
Dp	1200	TGTCAATGTCTGAAGTCCCAAGCGCAAGTTGGCCAAAGACGCCAAGGTGAGACGAGAAAG	1257

RESULT	4
ADP13278	
ID	ADP13278 standard; DNA; 4724 BP
XX	
AC	ADP13278;
XX	
DT	26-AUG-2004 (first entry)
XX	

DE Renal cell carcinoma differentially expressed gene #14.  
XX  
XX ds; diagnosis; non-blood disease; solid tumor; gene expression;  
XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
XX head/neck cancer; differential expression.  
XX  
XX Homo sapiens.  
XX  
XX WO2004048933-A2.  
XX  
XX 10-UN-2004.  
XX  
XX 21-NOV-2003; 2003WO-US037481.  
XX  
XX 21-NOV-2002; 2002US-0427982P.  
XX PR 03-APR-2003; 2003US-0459782P.  
XX  
XX (AMBP ) WYETH.  
XX PA (TWIN/) TWINE N C.  
XX PA (BURC/) BURCZYNSKI M E.  
XX PA (TREP/) TREPICCHIO W L.  
XX PA (DORN/) DORNER A.  
XX PA (STOV/) STOVER J A.  
XX PA (SLON/) SLONI D K.  
XX  
XX  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
XX Sloni DK;  
XX  
XX WPI; 2004-460799/43.  
XX  
XX  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
XX differential expression profile of specific genes in peripheral blood  
XX sample of subject with reference expression profile of specific genes.  
XX  
XX Disclosure; SEQ ID NO 14; 350bp; English.  
XX  
XX  
XX The invention relate to a method of diagnosing (M1) non-blood disease  
XX such as solid tumor by providing peripheral blood sample of human having  
XX non-blood disease, and comparing an expression profile of specific genes  
XX in the peripheral blood sample to reference expression profile of the  
XX genes, where each of the genes is differentially expressed in peripheral  
XX blood mononuclear cells (PBMCs) of patients having the disease as  
XX compared to PBMCs of normal humans. The method is useful for diagnosing  
XX non-blood disease such as solid tumor. The solid tumor is chosen from  
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood  
XX sample is a whole blood sample (claimed). (M1) is useful for identifying  
XX genes that are differentially expressed in peripheral blood samples  
XX isolated at different stages of progression, development or treatment of  
XX RCC and/or other solid tumors. This sequence corresponds to a gene that  
XX is differentially expressed and detected by the method of the invention.  
XX (Note: this sequence is not given as part of the printed specification  
XX but was obtained from WIPO in electronic format at  
XX ftp.wipo./pub/published\_pct\_sequences).

Qy	276	TTGGCCCTCCCTTAAATATCTCAAGAAGATGACACTCTGTGTGTGTGTAGTACCTCTAC	335
Db	180	TTGGCCCTCCCTTAAATATCTCAAGAAGATGACACTCTGTGTGTGTAGTACCTCTAC	239
Qy	336	TTTTATGGAAATCCCTGCMAAGTGAATGCCCTCAAAAGCGTCCGATGACTGGGGACTGACACC	395
Db	240	TTTTATGGAAATCCCTGCMAAGTGAATGCCCTCAAAAGCGTCCGATGACTGGGGACTGACACC	299
Qy	396	ATGAGGCAAAATCCCAAGTGTGTAAGATGAGCAGCTGCATCAAGTGGCCACTCTTGAA	455
Db	300	ATGAGGCAAAATCCCAAGTGTGTAAGATGAGCAGCTGCATCAAGTGGCCACTCTTGAA	359
Qy	456	CACCTCTTTGAATTCACCTAAGACAGACCCATTACAGTGGCCCTAATCTGTATCTGTGAT	515
Db	360	CACCTCTTTGAATTCACCTAAGACAGACCCATTACAGTGGCCCTAATCTGTATCTGTGAT	419
Qy	516	TGACATAGCAGGACCGGACCTTGAGAGGCCAATTAACTTCGCGCTCCCGAAGCCG	575
Db	420	TGACATAGCAGGACCGGACCTTGAGAGGCCAATTAACTTCGCGCTCCCGAAGACCGC	479
Qy	576	ATTGTAGAGGAAAGATGATGCTGTGTTCCGGGCCACTCTCCCTCAATGACACTGGGCAC	635
Db	480	ATTGTAGAGGAAAGATGATGCTGTGTTCCGGGCCACTCTCCCTCAATGACACTGGGCAC	539
Qy	636	TATACCTGCATGTTAAGAACACTACATATTTGCAGCAAAAGTTGCATTTCCCTGGAAGTT	695
Db	540	TATACCTGCATGTTAAGAACACTACATATTTGCAGCAAAAGTTGCATTTCCCTGGAAGTT	599
Qy	696	GTTCAAAAAGACAGTGTGTTCAATTCGCCCAATGAAACCTCCAGTGCATPAACTGATATA	755
Db	600	GTTCAAAAAGACAGTGTGTTCAATTCGCCCAATGAAACCTCCAGTGCATPAACTGATATA	659
Qy	756	GAATATGSCATTCAAGAGATCACTTGTCCAATGTAGTGAATTTTCTTCCATGCTC	815
Db	660	GAATATGSCATTCAAGAGATCACTTGTCCAATGTAGTGAATTTTCTTCCATGCTC	719
Qy	816	AAACCGAATACACTGTGTATATGSGGCTGTATPAAATACAGAAATTTAATPAGTATA	875
Db	720	AAACCGAATACACTGTGTATATGSGGCTGTATPAAATACAGAAATTTAATPAGTATA	779
Qy	876	CCCGAAGGTATGAACCTTAGTTTCTCTCATTCGCTTAATTTCAATATATGAAATTAACA	935
Db	780	CCCGAAGGTATGAACCTTAGTTTCTCTCATTCGCTTAATTTCAATATATGAAATTAACA	839
Qy	936	TGTGTGTATACATATCCAGAAATGGAAGTACGTTTATCTACACGAGACTGTGACTATA	995
Db	840	TGTGTGTATACATATCCAGAAATGGAAGTACGTTTATCTACACGAGACTGTGACTATA	899
Qy	996	AAGGTAGTAGCTCTCCAAAAAATGCAGTGCCTCCGTGATTCATTCACTPATATGATCAT	1055
Db	900	AAGGTAGTAGCTCTCCAAAAAATGCAGTGCCTCCGTGATTCATTCACTPATATGATCAT	959
Qy	1056	GTGTCCTATGGAAGAAACACAGAGAGAGAGTACATCTCCCTGATAGGCTATATTTAGT	1115
Db	960	GTGTCCTATGGAAGAAACACAGAGAGAGAGTACATCTCCCTGATAGGCTATATTTAGT	1015
Qy	1116	TTTCTGATGATTTCTCGCAATGAGGTTTGTGTGACCATTTGATGAAAAAAACCTGATGAC	1175
Db	1020	TTTCTGATGATTTCTCGCAATGAGGTTTGTGTGACCATTTGATGAAAAAAACCTGATGAC	1079
Qy	1176	ATACACTATGATGATCAGCATTACAGAAAGTTAATGCTATAGTAAACAGAAATGAAACT	1235
Db	1080	ATACACTATGATGATCAGCATTACAGAAAGTTAATGCTATAGTAAACAGAAATGAAACA	1133
Qy	1236	AGAACTCGATTTTGGAGCATCAAGAAAGTTAATCTGAGGATCTTAAGCGCATATGTC	1295
Db	1140	AGAACTCGATTTTGGAGCATCAAGAAAGTTAATCTCTGAGGATCTTAAGCGCATATGTC	1199
Qy	1286	TGTCACTGTAGAAAGTCCAAAGGCGCAAGTGTGCACAGACGCCAAGTGAAGACGAAGAAG	1353
Db	1200	TGTCACTGTAGAAAGTCCAAAGGCGCAAGTGTGCACAGACGCCAAGTGAAGACGAAGAAG	1257

XX	RESULT 5
ID	AAS15608
XX	AAS15608 standard; cDNA; 1740 BP.
AC	AAS15608;
DT	21-MAY-2002 (first entry)
XX	
XX	Human interleukin-1 Receptor accessory protein (IL-1R acp) cDNA.
DE	
XX	IL-1R acp; human; interleukin-1 receptor accessory protein; NF-kappaB;
XX	IL-1; IL-1RI; ss; inflammatory response.
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	CDS 10..1722
FT	/tag= a
FT	/product= "IL-1 Receptor accessory protein"
PX	
PN	US6280955-B1.
XX	
PD	28-AUG-2001.
XX	
PF	16-DEC-1997; 97US-00991944.
XX	
PR	16-DEC-1997; 97US-00991944.
PA	(TULAR-) TULARIK INC.
P1	
P1	Cao Z;
DR	WPI; 2001-595441/67.
DR	P-RSDB; AAU09966.
PT	
PT	Isolated polypeptide designated interleukin receptor accessory
XX	polypeptide is useful for regulating cell function.
PS	
PS	Claim 11; Fig 2; 21pp; English.
CC	This sequence represents the human interleukin-1 receptor accessory
CC	protein (IL-1RaCP) cDNA of the invention. The interleukin receptor
CC	accessory protein (IL-1RaCP) and its modulators (agonists/antagonists)
CC	are useful for regulating cell function. Transient expression of either
CC	IL-1RI or IL-1RaCP alone does not result in ligand-independent induction
CC	of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
CC	coexpression of both proteins resulted in a 20-fold increase in
CC	activation of NF-kappaB activity to a level comparable to that induced by
CC	IL-1. These data suggest that aggregation of IL-1RI and IL-1RaCP as a
CC	result of protein overexpression can elicit a signaling pathway leading
CC	to NF-kappaB activation. Modulation of signal transduction involving NF-
CC	kappaB in a cell may be achieved by modulating the activity of IL-1RaCP
CC	using binding agents such as agonists and antagonists. Hybridisation
CC	probes to the cDNA sequence can be used to identify wild-type and mutant
CC	IL-1RaCP alleles in clinical and laboratory samples. Mutant alleles are
CC	used to generate allele-specific oligonucleotide (ASO) probes for high-
CC	throughput clinical diagnoses of diseases or disorders with an
CC	inflammatory response. In therapy, therapeutic IL-1RaCP nucleic acids are
CC	used to modulate cellular expression or intracellular concentration or
CC	availability of active IL-1RaCP. This invention also comprises a method
CC	of screening for an agent that modulates the interaction of an
CC	interleukin receptor accessory polypeptide (IL-1RaCP) to a binding target
XX	
SQ	Sequence 1740 BP; 518 A; 360 C; 411 G; 451 T; 0 U; 0 Other:
Query Match	49.0%; Score 1056.8; DB 5; Length 1740;
Best Local Similarity	99.8%; Pred. No. 2.4e-236;
Matches 1058; Conservative	0; Mismatches 2; Indels 0; Gaps 0
DG	294 TCTCAAGATACACTTCGTGGCGGTGTAGATGCTCCTAACTTTATGGAATCTGCAG 353
1 TCTCAAGAATACACTTCGTGGCGGTGTAGATGCTCCTAACTTTATGGAATCTGCAG 60	

QY	354	AGTGTGCTCGAAGCGCTGCATACACTGGGACCTAGACACCATGAGGCAATCCAAAGT	413
Db	61	AGTATGCTCTAGAACGCTGGCGATGACTGGGACCTAGACACCATGAGGCAATCCAAAGT	120
QY	414	TTTGAAGATGAGCCAGCTCGCATCAAGTCCCATCTTTTGAACATCTTGTGAATTAAC	473
Db	121	TTTGAAGATGAGCCAGCTCGCATCAAGTCCCATCTTTTGAACATCTTGTGAATTAAC	180
QY	474	TACACACAGCCCATTCAGCTGCGCTTACTCGATCTGGTATGTGACTAGACGACGG	533
Db	181	TACACACAGCCCATTCAGCTGCGCTTACTCGATCTGGTATGTGACTAGACGACGG	240
QY	534	GACCTTGAGAGCCCAATTAACTTCGCGCTCCCCGAAACCGCATTAGTAAGAGAAAT	593
Db	241	GACCTTGAGAGCCCAATTAACTTCGCGCTCCCCGAAACCGCATTAGTAAGAGAAAT	300
QY	594	GTGCTGTGGTTCGGGCGCCACTCTCTCTCAATGACCTGGCACTTAATCTGTCATGTTAAG	653
Db	301	GTGCTGTGGTTCGGGCGCCACTCTCTCTCAATGACCTGGCACTTAATCTGTCATGTTAAG	360
QY	654	AACACTACATATTGAGCAGCAAGTTCATTCCTCTGGAAGTGTTCAAAAGACAGCTGT	713
Db	361	AACACTACATATTGAGCAGCAAGTTCATTCCTCTGGAAGTGTTCAAAAGACAGCTGT	420
QY	714	TTCAATTCGCCCATGAACTCCCACTGCTAACTGATATAGATATGCAATTCAGAG	773
Db	421	TTCAATTCGCCCATGAACTCCCACTGCTAACTGATATAGATATGCAATTCAGAG	480
QY	774	ATCACTTGCCCAAGTATGATGATATTTTCCCTCGAGTCAAAACCGACTATGACTGG	833
Db	481	ATCACTTGCCCAAGTATGATGATATTTTCCCTCGAGTCAAAACCGACTATGACTGG	540
QY	834	TATATGGCGTGTATATAATACAGATTTTAAATGATATACCCGAAAGTATGAACCTG	893
Db	541	TATATGGCGTGTATATAATACAGATTTTAAATGATATACCCGAAAGTATGAACCTG	600
QY	894	AGTTTCCTCATTTGCCCTTAATTTCAATATATGGAATTTACACTGTGTGTTACATATCA	953
Db	601	AGTTTCCTCATTTGCCCTTAATTTCAATATATGGAATTTACACTGTGTGTTACATATCA	660
QY	954	GAAATGAGCGTACGTTTCATCTCACAGGACTCTGACTGTAAAGTATGAGTCTCTCCA	1013
Db	661	GAAATGAGCGTACGTTTCATCTCACAGGACTCTGACTGTAAAGTATGAGTCTCTCCA	720
QY	1014	AAAAATGAGTGCCTCTGTGATCCATTTACCTAATATGATCATGTGCTTATGAGAAAGA	1073
Db	721	AAAAATGAGTGCCTCTGTGATCCATTTACCTAATATGATCATGTGCTTATGAGAAAGA	780
QY	1074	CCAGGAGAGAGCTACTCATTCCTCGTACGGGTATTTTATGTTTCTGATGATCTCTGC	1133
Db	781	CCAGGAGAGAGCTACTCATTCCTCGTACGGGTATTTTATGTTTCTGATGATCTCTGC	840
QY	1134	AATGAGGTTTGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTAC	1193
Db	841	AATGAGGTTTGGTGGACCATTTGATGAAAAAAACCTGATGACATCACTATTGATGTAC	900
QY	1194	ATTAAACGAAATGATATAGCTATAGTGAACAGAAATGAATCTAGAACTCAATTTTGGC	1253
Db	901	ATTAAACGAAATGATATAGCTATAGTGAACAGAAATGAATCTAGAACTCAATTTTGGC	960
QY	1254	ATCAAGAAAGTTACTCTGAGGATCTCAAGCGCACTATGTCTGCATGCTGAAGTACC	1313
Db	961	ATCAAGAAAGTTACTCTGAGGATCTCAAGCGCACTATGTCTGCATGCTGAAGTACC	1022
QY	1314	AAAGGCGAAGTTGCCAATAGCAGCCCAAGTGAAACAGAAAG	1353
Db	1021	AAAGGCGAAGTTGCCAATAGCAGCCCAAGTGAAACAGAAAG	1060

AC	ABX12962;	
XX		
DT	10-MAY-2003	(first entry)
XX		
DE	DNA encoding human soluble IL-1 receptor type 1.	
XX		
KW	Interleukin 1; human; interleukin1; IL-1; IL-1-receptor; IL-1R; ds;	
XX	IL-R accessory protein; IL-RacP; protein-protein interaction; gene.	
OS	Homo sapiens.	
PN	GB2375604-A.	
PD	20-NOV-2002.	
XX		
PF	18-MAY-2001; 2001GB-00012251.	
XX		
PR	18-MAY-2001; 2001GB-00012251.	
XX		
PA	(WARN ) WARNER LAMBERT CO.	
PI	Bertelli F, Brown JP, Gee NS;	
XX		
PT	WPI, 2003-150708/15.	
DR	P-PsDB; AB008133.	
XX		
PT	Determining ability of test compound to modulate formation of interleukin	
XX	soluble trimolecular complex, by bringing into contact the components of	
XX	the complex and test compound and determining amount of complex formed.	
XX		
XX	Example 2; Page 150-151; 171pp; English.	
XX		
XX	This invention relates to a novel assay for determining the ability of a	
XX	test compound to modulate the formation of a trimolecular complex (TC)	
CC	including interleukin (IL), a soluble IL-receptor (IL-R) polypeptide and	
CC	a soluble IL-R accessory protein (IL-RacP). The method comprises bringing	
CC	into contact an IL polypeptide, a soluble IL-R polypeptide, a soluble IL-	
CC	RacP polypeptide and a test compound, and determining the amount of TC	
CC	formed. The method of the invention is useful for determining the ability	
CC	of a test compound to modulate the formation of a trimolecular complex	
CC	including IL, a soluble IL-R and a soluble IL-RacP. The method is useful	
CC	for high throughput screening and enables direct measurement of protein	
CC	binding characteristics. It is also useful for identifying small molecule	
CC	inhibitors of TC and hence of IL-1 biological activity. The method may be	
CC	used in screening methods and assays for agents which modulate the	
CC	interaction between IL and IL-R, and/or the interaction between IL-RacP	
CC	and the IL-R/IL biomolecular complexes. This method identifies small	
CC	molecule inhibitors of TC and hence IL-1 biological activity, and	
CC	provides a significant advantage over prior methods since it is possible	
CC	to dose orally and to reduce the cost of production of such compounds	
CC	compared to the production cost of recombinant proteins. The main	
CC	advantage of using soluble forms of the proteins in the method is the	
CC	ease with which these reagents enable the formatting and running of High	
CC	Throughput Screening (HTS) assays. The present sequence represents a DNA	
CC	sequence encoding an interleukin 1 family protein used in the method of	
CC	the invention	
XX		
XX	Sequence 1713 BP; 504 A; 358 C; 404 G; 447 T; 0 U; 0 Other;	
XX		
XX	Query Match	48.6%; Score 1047.8; DB 8; Length 1713;
XX	Best Local Similarity	99.8%; Pred. No. 3e-234;
XX	Matches 1049; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	303	ATGACACTTCTGTGTGTGTGTGTGTGTGTGTCTTACTCTTTATGTGAATTCCTGCAAGTGATGCC 362
DB	1	ATGACACTTCTGTGTGTGTGTGTGTGTGTGTCTTACTCTTTATGTGAATTCCTGCAAGTGATGCC 60
QY	363	TCAGAACGCTGCATGTACTGGGAGACTGAGACCAACATGAGGCAAAATCCAGTGTGTAAGAT 422
DB	61	TCAGAACGCTGCATGTACTGGGAGACTGAGACCAACATGAGGCAAAATCCAGTGTGTAAGAT 120
QY	423	GAGCGAGTGGCATCAAGTGGCCCACTCTTTGAACACTTTTGAATTCAACTACGACACA 482

Db 121 GAGCAGCTCGCATGAGTGGCCCACTCTTTGAAACCTTTGAAATTCACCTACAGACA 180  
 Qy 483 GCCCATTCAGCTGGCTTACTCTGTATCTGTATTTGATTAAGACGACCGGACCTTGAG 542  
 Db 181 GCGCATTCAGCTGGCTTACTCTGTATTTGATTAAGACGACCGGACCTTGAG 240  
 Qy 543 GAGCAATTAATCTTCCGCTCCCGGAGAACGCAATTAAGAGAAAGATGTCTGTG 602  
 Db 241 GAGCAATTAATCTTCCGCTCCCGGAGAACGCAATTAAGAGAAAGATGTCTGTG 300  
 Qy 603 TTCCGCGCCACTCTCTCAATGACACTGGCAACTATACCTCATGTTAAGAACACTACA 662  
 Db 301 TTCCGCGCCACTCTCTCAATGACACTGGCAACTATACCTCATGTTAAGAACACTACA 360  
 Qy 663 TATTGCAAGAAAGTGGCAATTTCCCTGGAAAGTGTGCAAAAGAGAGTGTTCATTC 722  
 Db 361 TATTGCAAGAAAGTGGCAATTTCCCTGGAAAGTGTGCAAAAGAGAGTGTTCATTC 420  
 Qy 723 CCATGAAATCTCCAGTCATTAATCTGTATAGAAATGGCAATTCAGAGATCACTGT 782  
 Db 421 CCATGAAATCTCCAGTCATTAATCTGTATAGAAATGGCAATTCAGAGATCACTGT 480  
 Qy 783 CCAAAATGATGATGATTTTCTTCCAGTGTCAAAAGGACTATTCACCTGTGATATG 842  
 Db 481 CCAAAATGATGATGATTTTCTTCCAGTGTCAAAAGGACTATTCACCTGTGATATG 540  
 Qy 843 TGTATTAATTAATGATTTTATATGTAATACCCGAGGTATGAACTTGAATTCCTC 902  
 Db 541 TGTATTAATTAATGATTTTATATGTAATACCCGAGGTATGAACTTGAATTCCTC 600  
 Qy 903 ATTGCCTTAATTTCAATTAATGAAATTTACACATGTGTTTACATATCCGAAATG 962  
 Db 601 ATTGCCTTAATTTCAATTAATGAAATTTACACATGTGTTTACATATCCGAAATG 660  
 Qy 963 CCTAGTTTCACTGACGAGACTGTGCTGTAAGAGTATGAGGCTCCCAAAATGCA 1022  
 Db 661 CCTAGTTTCACTGACGAGACTGTGCTGTAAGAGTATGAGGCTCCCAAAATGCA 720  
 Qy 1023 GTGCCCCCTGTATCTCACTTAATGATCAATGTGTATGAGAAAGAACGAGAG 1082  
 Db 721 GTGCCCCCTGTATCTCACTTAATGATCAATGTGTATGAGAAAGAACGAGAG 780  
 Qy 1083 GAGCTACTCATCTCCCTGTAGAGTCTATTTTGTTCGATGAGATTCGGAATGAGGT 1142  
 Db 781 GAGCTACTCATCTCCCTGTAGAGTCTATTTTGTTCGATGAGATTCGGAATGAGGT 840  
 Qy 1143 TCGTGAACCATGATGAGAAAGAAACCTGATGACATCACTATTGATGTCACCATTA 1202  
 Db 841 TCGTGAACCATGATGAGAAAGAAACCTGATGACATCACTATTGATGTCACCATTA 900  
 Qy 1203 AGTATTAAGTCATGATGAGAAAGAAAGATGAATGAATCTGATTTTGTAGCATCA 1262  
 Db 901 AGTATTAAGTCATGATGAGAAAGAAAGATGAATGAATCTGATTTTGTAGCATCA 960  
 Qy 1263 GTTACCTCTGAGAGATCTCAAGCGAGCTATGCTGATGCTGATGAGAGCGAA 1322  
 Db 961 GTTACCTCTGAGAGATCTCAAGCGAGCTATGCTGATGCTGATGAGAGCGAA 1020  
 Qy 1323 GTTGCCTAAGCAGCAAGGTGAGCAAG 1353  
 Db 1021 GTTGCCTAAGCAGCAAGGTGAGCAAG 1051

RESULT 7  
 ABQ81182  
 ID ABQ81182 standard; cDNA; 2064 BP.  
 XX  
 AC ABQ81182;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Human IL-1 receptor accessory protein splice variant coding sequence.  
 XX

KM Interleukin-1; receptor; accessory protein; IL-1R ACP; splice variant;  
 KW human; immunosuppressive antiinflammatory; antitumor;  
 KM single nucleotide polymorphism; SNP; Gene; ss.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..2064  
 FT /tag= a  
 FT /product= "IL-1R ACP"  
 FT sig\_peptide 1..51  
 FT /tag= b  
 FT mat\_peptide 52..2061  
 FT /tag= c  
 FT variation replace(1792,C)  
 FT /tag= d  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT /frequency= "0.50"  
 XX  
 XX MO200264630-A2.  
 XX  
 XX 22-AUG-2002.  
 XX  
 XX 26-OCT-2001; 2001MO-US051060.  
 XX  
 XX 31-OCT-2000; 2000US-0244831P.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Sims JE, Smith DE;  
 XX WPI, 2002-657584/70.  
 XX P-PSDB; ABB79891.  
 DR  
 XX  
 XX New interleukin 1 (IL-1) Receptor Accessory Protein (IL-1R ACP) splice  
 PT variant protein, useful for screening for modulators of IL-1, or for  
 PT treating or preventing e.g. Crohn's disease, ulcerative colitis or  
 PT ulcers.  
 PT  
 XX  
 XX  
 XX Claim 1; Page 3-4; 60pp; English.  
 PS  
 XX  
 XX The present sequence is the coding sequence of a human interleukin 1 (IL-  
 CC 1) receptor accessory protein (IL-1R ACP) splice variant. This native  
 CC human sequence includes a polymorphism at an approximately 50/50 ratio.  
 CC This exists as an A or C at position 1792 of the coding sequence.  
 CC resulting in Thr or Pro at position 598 of the IL-1R ACP protein (see  
 CC ABB79891). The IL-1R ACP splice variant protein is a type I transmembrane  
 CC protein that is homologous to IL-1R type I. It shares 83% amino acid  
 CC identity with a previously described human IL-1R ACP, of which it is a  
 CC splice variant having an alternative cytoplasmic domain C-terminal  
 CC sequence (amino acids 449-687). Polymorphisms comprising the present  
 CC sequence in which nucleotide 1792 is A or C, and which encode  
 CC polypeptides comprising amino acids 384-687, 379-687 or 449-687 of human  
 CC IL-1R ACP splice variant, or a polypeptide that interacts with a signal  
 CC transduction factor, where amino acid 598 is Thr or Pro, are claimed, as  
 CC well as the encoded polypeptides, antibodies, a process for preparing the  
 CC polypeptides, and a method of using the polypeptides to screen for an  
 CC agonist or antagonist of IL-1. Agonists or antagonists of IL-1 are useful  
 CC for treating inflammatory diseases (e.g. rheumatoid arthritis or  
 CC inflammatory bowel disease), osteoporosis, autoimmune disease, Crohn's  
 CC disease, ulcerative colitis, idiopathic gastroparesis, pancreatitis, or  
 CC ulcers  
 CC  
 XX  
 XX Sequence 2064 BP; 585 A; 463 C; 476 G; 540 T; 0 U; 0 Other;  
 SO  
 Query Match 48.6%; Score 1047.8; DB 6; Length 2064;  
 Best Local Similarity 99.8%; Pred. No. 3.2e-234;  
 Matches 1049; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 303 ATGACACTCTGTGTGTGATGATGATCTCTCTTTATGAAATCTCGAAAGTATGCC 362  
 Db 1 ATGACACTCTGTGTGTGATGATGATCTCTCTTTATGAAATCTCGAAAGTATGCC 60

QY	36	TCGAAAGCGTGCATATCGGGGACTAGACACATGAGGGCAATCTCAAGTCTTGAAGAT	422
Db	61	TCGAAAGCGTGCATATCGGGGACTAGACACATGAGGGCAATCTCAAGTCTTGAAGAT	120
QY	423	GAGCGAGCTGGCATCAAGTGGCCACTCTTGAACCTCTTGAANTCACTAAGACA	442
Db	121	GAGCGAGCTGGCATCAAGTGGCCACTCTTGAACCTCTTGAANTCACTAAGACA	180
QY	483	GCCCATTCAGCTGGCCTTACTCTGATCTGTATTTGAGCTTAAGCAGGAGCCGGACCTTGAG	542
Db	181	GCCCATTCAGCTGGCCTTACTCTGATCTGTATTTGAGCTTAAGCAGGAGCCGGACCTTGAG	240
QY	543	GAGCGAATTACCTTCGGCTCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGTCTGTGG	602
Db	241	GAGCGAATTACCTTCGGCTCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGTCTGTGG	300
QY	603	TTCCGGGCGCACTTCCTCAATGACACTGGCACTATACCTGCATGTTAAGGACACTACA	662
Db	301	TTCCGGGCGCACTTCCTCAATGACACTGGCACTATACCTGCATGTTAAGGACACTACA	360
QY	663	TATTGCAAGCAAGTGTCAATTCCTCTTGGAGATTTGTTAAAAGACAGCTGTTCAATTC	722
Db	361	TATTGCAAGCAAGTGTCAATTCCTCTTGGAGATTTGTTAAAAGACAGCTGTTCAATTC	420
QY	723	CCCATGAACTCCAGTGCATAACTGTATATAGAAATGAGCATTCAGAGGATCACTGT	782
Db	421	CCCATGAACTCCAGTGCATAACTGTATATAGAAATGAGCATTCAGAGGATCACTGT	480
QY	783	CCAAATGATAGATATTTTCCCTTCAAGTCAAAACCGACTATCACTGTATATGGGC	842
Db	481	CCAAATGATAGATATTTTCCCTTCAAGTCAAAACCGACTATCACTGTATATGGGC	540
QY	843	TGTTATAAAAATAGAAATTTTAATATATGTAAATACCGGAGATGAACTTGAGTTCTC	902
Db	541	TGTTATAAAAATAGAAATTTTAATATATGTAAATACCGGAGATGAACTTGAGTTCTC	600
QY	903	ATTGCTTAATTTCAAAATATAGAAATTCACATGTGTGTTACATATCCGAAATATGA	962
Db	601	ATTGCTTAATTTCAAAATATAGAAATTCACATGTGTGTTACATATCCGAAATATGA	660
QY	963	CGTAGCGTTTCATCTCACACAGGACTGTGACTGTAAAGTAGTAGGCTCCCAAAAATATGA	102
Db	661	CGTAGCGTTTCATCTCACACAGGACTGTGACTGTAAAGTAGTAGGCTCCCAAAAATATGA	720
QY	1023	GTGCCCCCTGTGATCCATTCACTAATGATCATGTGTATGTAGAAAGAACAGAGAG	108
Db	721	GTGCCCCCTGTGATCCATTCACTAATGATCATGTGTATGTAGAAAGAACAGAGAG	780
QY	1083	GAGCTACTCAATCCCTGTACGGGCTATTTAGTTTTCGATGAGATTCGCAATGAGGTT	1144
Db	781	GAGCTACTCAATCCCTGTACGGGCTATTTAGTTTTCGATGAGATTCGCAATGAGGTT	840
QY	1143	TGTGTGACCAATTGATGAAAAAAACCTGTATGATCACTATATGATGTACCATTAAGAA	1204
Db	841	TGTGTGACCAATTGATGAAAAAAACCTGTATGATCACTATATGATGTACCATTAAGAA	900
QY	1203	AGTATATAGTCATATGTAGAACAGAAATGAAACTGAACTCGATTTTGAACATCAAGAA	126
Db	901	AGTATATAGTCATATGTAGAACAGAAATGAAACTGAACTCGATTTTGAACATCAAGAA	960
QY	1263	GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTGTAGAAATGTCCAAAGCGAA	1322
Db	961	GTTACTCTGAGGATCTCAAGCGCAGCTATGTCTGTCACTGTAGAAATGTCCAAAGCGAA	1022
QY	1323	GTTGCCAAAGCGCCAAAGGTGAAGAGAAAG	1353
Db	1021	GTTGCCAAAGCGCCAAAGGTGAAGAGAAAG	1051

AC	AATJ2027;
XX	
DT	14-OCT-1996    (first entry)
XX	
DE	Soluble interleukin-1 receptor accessory protein cDNA.
XX	
KW	Interleukin-1 receptor accessory protein; IL-1 antagonist; inflammation; therapy; anti-inflammatory; ss.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	sig_peptide 1..60
FT	*tag= a
FT	61..1077
FT	mac_peptide /tag= b
PX	
PN	WO9623067-A1.
PD	
DP	01-AUG-1996.
PF	
PI	17-JAN-1996;      96WO-EPOO0181.
PR	
PS	23-JAN-1995;      95US-00376268.  (HOFF ) HOFFMANN LA ROCHE & CO AG F. Chizomite RA, Ju GW; MPI: 1996-362691/36. P-PSEB; AAM01912.
PT	
PP	Isolated interleukin-1 receptor accessory protein - used to develop prods. to treat or prevent inflammatory or immunological activities of interleukin-1.
PS	Claim 9; Page 80-81; 115pp; English.
CC	
XX	
CC	A cDNA clone (AATJ2027) codes for a soluble form (AAM01912) of the human interleukin-1 receptor accessory protein (IL-IR AcP), a protein that inhibits the ability of IL-1 to bind to, or otherwise activate IL-IR, esp. the Type I IL-IR. It was obted. by PCR amplification (see also CG AATJ2029-30) of cDNA (AATJ2026) coding for the extracellular domain of IL- IR AcP (AAM01911). The soluble protein was expressed in Sf9 insect cells using a baculovirus system. It can be used to treat or prevent the inflammatory or immunological activities of IL-1, and also to screen for IL-1 antagonists
SC	Sequence 1077 BP; 326 A; 234 C; 232 G; 285 T; 0 U; 0 Other;
Query Match	48.5%; Score 1046.2; DB 2; Length 1077;
Best Local Similarity	99.7%; Pred. No. 5.9e-234;
Matches 1048; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	303 ATGACACTTGTGGTGAGTAGTGAAGTCCTACTTTATGGAATCCTGCAGAAGTATGCC 362
DB	1 ATGACACTTGTGGTGAGTAGTGAAGTCCTACTTTATGGAATCCTGCAGAAGTATGCC 60
OY	363 TCAGAACGCTGCGATGACTGGGAGCACTAGACCANTGAGGACAATCCAAGTTTTGAAGAT 422
DB	61 TCAGAAAGCTGCGATGACTGGGAGCATGACCACTGAGGACAATAATCCAAGTTTTGAAGAT 120
OY	423 GAGCGACTGCGATCAAGTGGCCACTCTTGAANAACATTCTTGAATCAAATACTAGACACA 482
DB	121 GAGCGACTGCGATCAAGTGGCCACTCTTGAANAACATTCTTGAATCAAATACTAGACACA 180
OY	483 GCCCATTCAGCTGGCCCTTAATCTTGATCTGTGATTTAGACTAAGCAGCACGGGACCTTGA 542
DB	181 GCCCATTCAGCTGGCCCTTAATCTTGATCTGTGATTTAGACTAAGCAGCACGGGACCTTGA 240
OY	543 GAGCAATTAATCTTCCGCCCTCCCAGAACCGCATTTAGTAAGGAAAAGATGTGCTGTGG 602
DB	241 GAGCAATTAATCTTCCGCCCTCCCAGAACCGCATTTAGTAAGGAAAAGATGTGCTGTGG 300

603 TTCCGGCCCACTCTCCATGATGACATGCGCACTATACCTGATGTTAAGGAACATACATA 662  
 Db TTCCGGCCCACTCTCCATGATGACATGCGCACTATACCTGATGTTAAGGAACATACATA 360  
 663 TATTGACCAAAAGTTGCACTTTCCCTGGAAAGTTGTTCAAAAAGCAGCTGTTCAATTC 722  
 Db TATTGACCAAAAGTTGCACTTTCCCTGGAAAGTTGTTCAAAAAGCAGCTGTTCAATTC 420  
 723 CCCATGAACCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782  
 Db CCCATGAACCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 783 .CCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 842  
 Db .CCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 843 TGTATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902  
 Db TGTATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 903 ATTGCTTAAATTTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 962  
 Db ATTGCTTAAATTTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 963 CCGATGTTTCACTTCAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1022  
 Db CCGATGTTTCACTTCAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 1023 GTGCCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1082  
 Db GTGCCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 1083 GAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1142  
 Db GAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 1143 TGTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202  
 Db TGTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 1203 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262  
 Db AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 1263 GTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322  
 Db GTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
 1323 GTTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1383  
 Db GTTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1021  
 1021 GTTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1081

RESULT 9  
 ACC48599  
 ID ACC48599 standard; cDNA; 1077 BP.  
 XX  
 AC ACC48599;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Soluble interleukin-1 accessory protein coding sequence.  
 XX  
 KW Human; interleukin-1 accessory protein; IL-1AcP; antagonist;  
 XX anti-rheumatic; anti-arthritic; nocropic; neuroprotective; vasotropic;  
 XX cerebroprotective; cardiatic; anti-inflammatory; antiasthmatic; gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1-1077  
 CDS /tag= a  
 FT

FT /partial  
 FT /product= "Soluble IL-1AcP"  
 FT /note= "No stop codon"  
 PN MO2003014309-A2.  
 PD 20-FEB-2003.  
 XX 07-AUG-2002; 2002MO-US024948.  
 PF 07-AUG-2001; 2001US-0310789P.  
 PR (IMMUNEX CORP.  
 XX Sime JE, Smith DE;  
 XX MPI; 2003-256566/25.  
 DR P-PSDB; ABR41899.  
 XX  
 PT Treating interleukin (IL)-1-associated disorders such as rheumatoid  
 PT arthritis, myocardial infarction, inflammatory bowel disease, asthma  
 PT and/or pancreatitis, by administering IL-1 receptor and IL-receptor  
 PT accessory protein.  
 XX  
 PS Disclosure; Page 42-44; 45p; English.  
 XX  
 CC The present sequence is the coding sequence for a soluble form of human  
 CC interleukin-1 (IL-1) accessory protein (IL-1AcP). The invention is based  
 CC in part on the discovery that soluble IL-1AcP enhances the inhibitory  
 CC ability of IL-1 receptor (IL-1R) and particularly type II IL-1R. A method  
 CC is provided for treating disorders associated with IL-1-mediated  
 CC inflammatory or immunoregulatory reactions involving the administration  
 CC of an IL-1 antagonist or inhibitor. Preferred methods use a type II IL-1R  
 CC in a form that binds IL-1, including IL-1 beta and IL-1 alpha, in  
 CC combination with IL-1AcP in a form that enhances the binding of type II  
 CC IL-1R to IL-1 beta and IL-1 alpha. The combination results in an enhanced  
 CC ability of type II IL-1R to block IL-1 signal transduction, thereby  
 CC interrupting the proinflammatory and immunoregulatory effects of IL-1.  
 CC Preferred forms of IL-1AcP include the present soluble form or a  
 CC truncated fragment of it. The method can be used to treat a patient  
 CC afflicted with rheumatoid arthritis, Alzheimer's disease, stroke, head  
 CC trauma, myocardial infarction, heart failure, periodontal disease,  
 CC inflammatory bowel disease, asthma or pancreatitis (all claimed)  
 CC  
 XX  
 SQ Sequence 1077 BP; 326 A; 234 C; 232 G; 285 T; 0 U; 0 Other;

Query Match 48.5%; Score 1046.2; DB 9; Length 1077;  
 Best Local Similarity 99.7%; Pred. No. 5.9e-234;  
 Matches 1048; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 303 ATGACACTTCTGT 362  
 Db 1 ATGACACTTCTGT 60

QY 363 TCAGAACGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422  
 Db 61 TCAGAACGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

QY 423 GAGCCAGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482  
 Db 121 GAGCCAGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180

QY 483 GCCCATTCAGCTGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542  
 Db 181 GCCCATTCAGCTGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 543 GAGCCATTAATCTTCCGCTCCCGAGAACCGCATGATGATGATGATGATGATGATGATGATGAT 602  
 Db 241 GAGCCATTAATCTTCCGCTCCCGAGAACCGCATGATGATGATGATGATGATGATGATGATGAT 300

QY 603 TTCCGGCCCACTCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662  
 Db 301 TTCCGGCCCACTCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360



QY	663	TATTGCAGCAAGTGGCATTTCCCTGGAAAGTTGTTCAAAAAGACAGCTGTTTCATTTCC	722
Db	361	TATTGCAGCAAGTGGCATTTCCCTGGAAAGTTGTTCAAAAAGACAGCTGTTTCATTTCC	420
QY	723	CCCATGAAGACTCCCGAGTGCATAAACTGTATATAGAAATAGCATTCAGAGATCACTGT	782
Db	421	CCCATGAAGACTCCCGAGTGCATAAACTGTATATAGAAATAGCATTCAGAGATCACTGT	480
QY	783	CCAAATGTAGATGGATATTTTCCCTCCAGTGCAAACCGACTATCACTTGGTATATGGCC	842
Db	481	CCAAATGTAGATGGATATTTTCCCTCCAGTGCAAACCGACTATCACTTGGTATATGGCC	540
QY	843	TGTTATATAAATACAGAAATTTTAATATATATATACCCGAAAGATGAACTTAGTTCCCTC	902
Db	541	TGTTATATAAATACAGAAATTTTAATATATATATACCCGAAAGATGAACTTAGTTCCCTC	600
QY	903	ATTGCTTTAATTTCAATTAATAGAAATTACAAGTGTGTTTAACTATCCGAAATATGA	962
Db	601	ATTGCTTTAATTTCAATTAATAGAAATTACAAGTGTGTTTAACTATCCGAAATATGA	660
QY	963	CGTACGTTTCAATCTACAGAGACCTGTGCTGTAAAGAGATAGGCTCCAAAAATATGA	1022
Db	661	CGTACGTTTCAATCTACAGAGACCTGTGCTGTAAAGAGATAGGCTCTCCAAAAATATGA	720
QY	1023	GTGCCCCCTGTGATCATTACCTTAATGATCATGTGTCATATGAGAAAGAACCGAGAG	1082
Db	721	GTGCCCCCTGTGATCATTACCTTAATGATCATGTGTCATATGAGAAAGAACCGAGAG	780
QY	1083	GAGCTACTCATTCCTCGTACAGTCTAATTTAGTTTCTCGATGAGANTCTCGAATAGAGGT	1142
Db	781	GAGCTACTCATTCCTCGTACAGTCTAATTTAGTTTCTCGATGAGANTCTCGAATAGAGGT	840
QY	1143	TGCTGAGACCATGTAGTGAAGAAAAAAACCTGATATACATCACTATTGATGTGCCATTAAAGAA	1202
Db	841	TGCTGAGACCATGTAGTGAAGAAAAAAACCTGATATACATCACTATTGATGTGCCATTAAAGAA	900
QY	1203	AGTATTAATCATATGTAAGAACAGAAATTAACCTAGAACTCAGATTTTGAAGATCAAGAAA	1262
Db	901	AGTATTAATCATATGTAAGAACAGAAATTAACAGAACTCAGATTTTGAAGATCAAGAAA	960
QY	1263	GTTACCTGTGAGATCTCAAGCGCAGCTATGTCTCATGTAGAAAGTGCAAAGCGCAA	1322
Db	961	GTTACCTGTGAGATCTCAAGCGCAGCTATGTCTCATGTAGAAAGTGCAAAGCGCAA	1020
QY	1323	GTTGCGAAAGCAGCCAGGTGATAGCAGAAAG	1353
Db	1021	GTTGCGAAAGCAGCCAGGTGATAGCAGAAAG	1051

RESULT 10  
AAT32026  
ID AAT32026 standard; cDNA; 1713 BP.

DT 14-OCT-1996 (first entry)

Human interleukin-1 receptor accessory protein cDNA.

**KW** Interleukin-1 receptor accessory protein; IL-1 antagonist; inflammation; therapy; antiinflammatory; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

	sig_peptide
FT	
FT	

mat\_peptide

AA  
PN W09623067-A1.

MO30623067-H1  
FN  
XX

PD 01-AUG-1996.

17-JAN-1996: 96WO-EP0000181.

23-JAN-1995: 95US-00376268.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F. RA

AA Chizomite BA. In GW.

XX WPB. 1996-362691 / 36  
DP

DR P-PSDB; AAM01911.  
XX

PT Isolated interleukin-1 receptor accessory protein - used to develop probes to treat or prevent inflammatory or immunological activities of

pt interleukin-1.

Claim 2; Page 71-72; 115pp; English.

CC A CDNA clone (AAT3302c) codes for human interleukin-1 receptor accessory  
CC protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind  
CC to or otherwise activate the IL-1R, esp. the Type I IL-1R. It was obtd.  
CC from a human YT cell CDNA library using a probe derived from a pure IL-1R  
CC partial genomic clone. The cDNA can be used for the prodn. of pure IL-1R  
CC AcP by expression in a host cell. The IL-1R AcP is used to treat or  
CC prevent the inflammatory or immunological activities of IL-1

Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 U; 0 Other;

Query Match 48.5%; Score 1046.2; DB 2; Length 1713;

```

Best local similarity  22.78; 1100; 100; 100; 100;
Matches 1048;  Conservati  0;  Mismatches  3;  Indels  0;  Gaps  0;

```

303 ATGACACTTCTGTGGTGTGTAAGTGAATCTTCTACTTTATGGAATCCTGCAAAAGTGATGCC 362

Db 1 ATGACACTTCTGTGGTGTGTAGTGAATCTCTACTTTTATGCAATCCTGCAAGTATGCC 60

363 TCAGAACGCTGCAGATGACTGGGACTAGACACCATGAGGCCAATCCAAGTGTTTGAAGAT 422

61 TTAGGACCGCTGCGATGACTGAGGACTTAGACACCATGAGGCAATCCAACTGTTTGAAGAT 120

[illegible][illegible][illegible]

100 240

[illegible]

\_\_\_\_\_

.....

100

1992

1. The first step in the process of creating a new product is to identify a market need. This involves conducting market research to understand what consumers want and what problems they are facing. Once a need is identified, the next step is to develop a concept that addresses this need. This is often done through brainstorming sessions with a team of designers and engineers. The concept is then refined through prototyping and testing, ensuring that it meets the requirements of the market. Finally, the product is launched into the market, and its performance is monitored to ensure it continues to meet the needs of consumers.

\_\_\_\_\_

[illegible][illegible]

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

QY 903 ATTGCTTAAATTTCAATATGAAATTAACATGCTGTTGTTAATATCCAGAAATGGA 962  
 DB 601 ATTGCTTAAATTTCAATATGAAATTAACATGCTGTTGTTAATATCCAGAAATGGA 660  
 QY 963 CGTAGCTTTCATCTCAGCAGAGCTGACCTGTAAGAGTAGAGCTCCCAAAAATGCA 1022  
 DB 661 CGTAGCTTTCATCTCAGCAGAGCTGACCTGTAAGAGTAGAGCTCCCAAAAATGCA 720  
 QY 1023 GTGCCCCCTGTGATCATTACCTATATGATGATGCTGTATGAGAAAGAACCCAGAGAG 1082  
 DB 721 GTGCCCCCTGTGATCATTACCTATATGATGATGCTGTATGAGAAAGAACCCAGAGAG 780  
 QY 1083 GAGCTACATCTTCCCTGTATGAGCTATTTTATTTTCTGAGAGATTCCTCCAGATGAGTT 1142  
 DB 781 GAGCTACATCTTCCCTGTATGAGCTATTTTATTTTCTGAGAGATTCCTCCAGATGAGTT 840  
 QY 1143 TGGTGGACCATTTGATGAGAAAGAACCTATATGATCATTATTTGATGAGAAAGAAC 1202  
 DB 841 TGGTGGACCATTTGATGAGAAAGAACCTATATGATCATTATTTGATGAGAAAGAAC 900  
 QY 1203 AGTATTAAGTCATGTAAGAACAGAGATGAACTGAACTGATTTTGAAGCATCAAGAA 1262  
 DB 901 AGTATTAAGTCATGTAAGAACAGAGATGAACTGAACTGATTTTGAAGCATCAAGAA 960  
 QY 1263 GTTACCTCTGAGAGATCTCAAGGAGAGCTATGCTGTATGCTAGAGAGCCAAAGCGAA 1322  
 DB 961 GTTACCTCTGAGAGATCTCAAGGAGAGCTATGCTGTATGCTAGAGAGAGCGAA 1020  
 QY 1323 GTTGGCAAAGCAGCCAGAGGTGAAAGCAGAAAG 1353  
 DB 1021 GTTGGCAAAGCAGCCAGAGGTGAAAGCAGAAAG 1051  
 RESULT 11  
 ID ACC48598 standard; cDNA, 1713 BP.  
 AC ACC48598;  
 XX  
 DT 11-AUG-2003 (first entry)  
 DE Human interleukin-1 accessory protein coding sequence.  
 XX  
 KW Human; interleukin-1 accessory protein; IL-1AcP; antagonist;  
 KW antirheumatic; antirheumatic; nocotropic; neutroprotective; vasotropic;  
 KW cerebroprotective; cardiant; antiinflammatory; antiaesthetic; gene; ss.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT 1..1713  
 FT CDS /\*tag= a  
 FT /\*product= "IL-1AcP"  
 FT  
 FN WO2003014309-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 07-AUG-2002; 2002MO-US024948.  
 XX  
 PR 07-AUG-2001; 2001US-0310789P.  
 XX  
 PA (IMMUNEX CORP.  
 PI Sims JE, Smith DE;  
 XX  
 DR MPI: 2003-255566/25.  
 DR P-PSDB; ABR41898.  
 XX  
 PT Treating interleukin (IL)-1-associated disorders such as rheumatoid  
 PT arthritis, myocardial infarction, inflammatory bowel disease, asthma  
 PT and/or pancreatitis, by administering IL-1 receptor and IL-1-receptor  
 PT accessory protein.

XX  
 PS Disclosure; Page 33-39; 45pp; English.  
 XX  
 CC The present sequence is the coding sequence for human interleukin-1 (IL-  
 CC 1) accessory protein (IL-1AcP). The invention is based in part on the  
 CC discovery that soluble IL-1AcP enhances the inhibitory ability of IL-1  
 CC receptor (IL-1R) and particularly type II IL-1R. A method is provided for  
 CC treating disorders associated with IL-1-mediated inflammatory or  
 CC immunoregulatory reactions involving the administration of an IL-1  
 CC antagonist or inhibitor. Preferred methods use a type II IL-1R in a form  
 CC that binds IL-1, including IL-1 beta and IL-1 alpha, in combination with  
 CC IL-1AcP in a form that enhances the binding of type II IL-1R to IL-1 beta  
 CC and IL-1 alpha. The combination results in an enhanced ability of type II  
 CC IL-1R to block IL-1 signal transduction, thereby interrupting the  
 CC proinflammatory and immunoregulatory effects of IL-1. Preferred forms of  
 CC IL-1AcP are soluble forms such as that given in ABR41898. The method can  
 CC be used to treat a patient afflicted with rheumatoid arthritis,  
 CC Alzheimer's disease, stroke, head trauma, myocardial infarction, heart  
 CC failure, periodontal disease, inflammatory bowel disease, asthma or  
 CC pancreatitis (all claimed).  
 XX  
 SQ Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 U; 0 Other;  
 Query Match 48.5%; Score 1046.2; DB 9; Length 1713;  
 Best Local Similarity 99.7%; Pred. No. 7.1e-234;  
 Matches 1048; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 303 ATGACACTTCTGTGCTGTATGAGTCTCTCTTTATGAAATGCTGAAAGTATGCC 362  
 DB 1 ATGACACTTCTGTGCTGTATGAGTCTCTCTTTATGAAATGCTGAAAGTATGCC 60  
 QY 363 TCAGAACGCTGCGATGACGCGGAGCTAGACACCATAGAGCAATCCAAAGTGTGAAGAT 422  
 DB 61 TCAGAACGCTGCGATGACGCGGAGCTAGACACCATAGAGCAATCCAAAGTGTGAAGAT 120  
 QY 423 GAGCCAGCTGCGATGACGCGGAGCTAGACACCATAGAGCAATCCAAAGTGTGAAGAT 482  
 DB 121 GAGCCAGCTGCGATGACGCGGAGCTAGACACCATAGAGCAATCCAAAGTGTGAAGAT 180  
 QY 483 GCCCATTCAGCTGCGCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 542  
 DB 181 GCCCATTCAGCTGCGCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 240  
 QY 543 GAGCCATTAATCTTCCGCTCTCCCGAAGACCCGATTAAGTACGAGAAAGTGTGCTGG 602  
 DB 241 GAGCCATTAATCTTCCGCTCTCCCGAAGACCCGATTAAGTACGAGAAAGTGTGCTGG 300  
 QY 603 TTCGGGCCCACTCTCTCTCAATGACCTGCGACATTAAGTACGAGAAAGTGTGCTGG 662  
 DB 301 TTCGGGCCCACTCTCTCTCAATGACCTGCGACATTAAGTACGAGAAAGTGTGCTGG 360  
 QY 663 TATTGAGCAAGATTGCTATTTCCCTTGGAGTGTTCAAAAGACAGCTGTTCAATTCC 722  
 DB 361 TATTGAGCAAGATTGCTATTTCCCTTGGAGTGTTCAAAAGACAGCTGTTCAATTCC 420  
 QY 723 CCCATGAATCTCCAGTGCATTAACCTGTATATAGAAATATGATGATCAAGATCACTTGT 782  
 DB 421 CCCATGAATCTCCAGTGCATTAACCTGTATATAGAAATATGATGATCAAGATCACTTGT 480  
 QY 783 CCATATGTATGATGATATTTCTTCCAGTGCATTAACCTGTATATAGAAATATGATGAT 842  
 DB 481 CCATATGTATGATGATATTTCTTCCAGTGCATTAACCTGTATATAGAAATATGATGAT 540  
 QY 843 TGTATTAATAATCAGAAATTTTATATATATATATATATATATATATATATATATATAT 902  
 DB 541 TGTATTAATAATCAGAAATTTTATATATATATATATATATATATATATATATATATATAT 600  
 QY 903 ATTGCTTAAATTTCAATATGAAATTAACATGCTGTTGTTAATATCCAGAAATGGA 962  
 DB 601 ATTGCTTAAATTTCAATATGAAATTAACATGCTGTTGTTAATATCCAGAAATGGA 660  
 QY 963 CGTAGCTTTCATCTCAGCAGAGCTGACCTGTAAGAGTAGAGCTCCCAAAAATGCA 1022

Db	661	CGTACGTTTCACTCACAGGACTCTGACTGAAAGGATGAGCTCTCCAAAATAATSCA	720
Qy	1023	GTGCCCCCTTGATATCCATTACCTATATATCATGTGTGCTATAGAAAAGAACCCGAGAG	1082
Db	721	GTGCCCCCTTGATATCCATTACCTATATATCATGTGTGCTATAGAAAAGAACCCGAGAG	780
Qy	1083	GAGCTACTCATTCCTGTGACGCTCATTTTATGTTTCTTGATGAGATTCCGCAATGAGGTT	1142
Db	781	GAGCTACTCATTCCTGTGACGCTCATTTTATGTTTCTTGATGAGATTCTCGCAATGAGGTT	840
Qy	1143	TGCTGACACCATTTGATGSAAAAAAACCCTGATGACATCACTATGTGATGTCACCATTAACGA	1202
Db	841	TGCTGACACCATTTGATGSAAAAAAACCCTGATGACATCACTATGTGATGTCACCATTAACGA	900
Qy	1203	AGTATTAAGTCAATAGTAGAACACAGACATGAAACTGAACTCAAGATTTTGAGCATCAGAA	1262
Db	901	AGTATTAAGTCAATAGTAGAACACAGACATGAAACTGAACTCAAGATTTTGAGCATCAGAA	960
Qy	1263	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCAATGCTAAGAAAGTGCACAAAGCGAA	1322
Db	961	GTTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCAATGCTAAGAAAGTGCACAAAGCGAA	1020
Qy	1323	GTTGCAAAAGCAGCCAGGTGATGAGCAGAAAG	1383
Db	1021	GTTGCAAAAGCAGCCAGGTGATGAGCAGAAAG	1081

XX	AA63748	ID	AA63748 standard; DNA; 2703 BP.
XX	AC	AAD63748;	
XX	DJ	12-FEB-2004	(first entry)
XX	DE	Human IL-1 Trap	823 DNA.
KM	KM	Cytokine; cytokine-related disease; immunomodulator; osteoporosis;	
KW	KW	cancer; cachexia; arthritis; cytostatic; osteopathic therapy; human	
RX	RX	gene; ds.	
OS	OS	Homo sapiens.	
XX	Key	location/Qualifiers	
FT	CD5	1..2703	
FT		/tag= a	
FT		/product= "Human IL-1 Trap protein"	
FT		1..1077	
FT		/tag= d	
FT		/note= "Human IL-1RAcP extracellular domain"	
FT		1..60	
FT		/tag= b	
FT		/label= Signal_peptide	
FT		61..2700	
FT		/tag= c	
FT		/product= "Human mature IL-1 Trap protein"	
FT		1078..2013	
FT		/tag= e	
FT		/note= "Human IL-1RI extracellular domain"	
FT		2014..2703	
FT		/tag= f	
FT		/note= "Human IgG1 CH2 and CH3 domain"	
XX	US2003143697-A1.		
XX	PN		
XX	PD	31-JUL-2003.	
XX	PF	28-OCT-2002; 2002US-00262162.	
XX	FR	22-SEP-1999; 99MO-USO22045.	
XX	PR	22-MAR-2001; 2001US-00787835.	
PA	(STAH/)	STAHL N.	

PA	(YANC//) YANCOPOULOS G D.
XX	
PI	Stahl N, Yancopoulos GD;
XX	
DR	WFI; 2003-851784/79.
DR	P-PSDB; ABW02185.
XX	
PT	New nucleic acid molecules encoding fusion polypeptides capable of
PT	binding a cytokine to form a non-functional complex, useful for treating
PT	cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
PT	or osteoporosis.
XX	
PS	Claim 4; Fig 41; 300pp; English.
XX	
CC	The present invention provides a novel fusion polypeptide capable of
CC	binding a cytokine to form a nonfunctional complex. The invention is
CC	useful for identifying agonists or antagonists of cytokine receptors and
CC	for treating cytokine-related diseases or disorders e.g. cancer,
CC	cachexia, arthritis and osteoporosis. The present sequence is human IL-1
CC	trap DNA
XX	
SQ	Sequence 2703 BP; 821 A; 627 C; 612 G; 643 T; 0 U; 0 Other;
Query Match	48.4%; Score 1043; DB 10; Length 2703;
Best Local Similarity	99.5%; Pred. No. 4.7e-233;
Matches 1046; Conservative	0; Mismatches 5; Indels 0; Gaps 0;

[illegible]



D <b>b</b>	661	CGTACGTTTCATCTCACCAGCACTGTGACTGTAAGAAGTAGTAGGCTCTCCAAAAATGCA	720
Q <b>y</b>	1023	GTGGCCCCCTGATGCCATTTCACACCTPAATGATCATGTGGCTCATGANAAGAACCCAGAAAG	1088
D <b>b</b>	721	GTGGCCCCCTGATGCCATTTCACACCTPATATCATGTGGCTCATGANAAGAACCCAGAAAG	780
Q <b>y</b>	1083	GAGCTACTCATCTCCCTGTGACGTCATTTTATGTTTGTCATGAGGAATTCGCAGTAGGTT	1144
D <b>b</b>	781	GAGCTACTCATCTCCCTGTGACGTCATTTTATGTTTGTCATGAGGAATTCGCGAATAGGTT	840
Q <b>y</b>	1143	TGATGACCAATTGATGGAATAAAAACCTGATGACATCATATTGATGATGCCATTAAACA	1202
D <b>b</b>	841	TGATGACCAATTGATGGAATAAAAACCTGATGACATCATATTGATGATGCCATTAAACA	900
Q <b>y</b>	1203	AGTATTAAGTCACTAGTAGACACGAAGATGAACCTAGAACTCAGATTTTGAGCATCAAGAA	1262
D <b>b</b>	901	AGTATTAAGTCACTAGTAGACACGAAGATGAACCAAGAACTCAGATTTTGAGCATCAAGAA	960
Q <b>y</b>	1263	GTTCACCTCTGAGGATCTCCAAAGCGACGTAATGTGTCTATGCTAAGAAAGTCCAAAGCGAA	1322
D <b>b</b>	961	GTTCACCTCTGAGGATCTCCAAAGCGACGTAATGTGTCTATGCTAAGAAAGTCCAAAGCGAA	1020
Q <b>y</b>	1323	GTTCACCAAGCAGCCAGGTAGAGCAAAAG	1353
D <b>b</b>	1021	GTTCACCAAGCAGCCAGGTAGAGCAAAAG	1051

RESULT 14

ID AAD63772 standard; DNA; 2709 BP.  
 XX  
 AC AAD63772;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human IL-1 Trap 823 mutant DNA #2.  
 XX  
 KW Cytokine; cytokine-related disease; immunomodulator; osteoporosis;  
 XX cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human;  
 KM mutant; mutcin; gene; ds.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 PN US2003143697-A1.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 28-OCT-2002; 2002US-00282162.  
 XX  
 PR 22-SEP-1999; 99MO-US022045.  
 XX  
 PR 22-MAR-2001; 2001US-00787835.  
 XX  
 PA (STAHL) STAHL N.  
 PA (YANC/) YANCOPOULOS G D.  
 PI Stahl N, Yancoopoulos GD;  
 DR WPI; 2003-851784/79.  
 XX  
 PT New nucleic acid molecules encoding fusion polypeptides capable of  
 PT binding a cytokine to form a non-functional complex, useful for treating  
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis  
 PT or osteoporosis.  
 XX  
 PS Claim 38; Page; 300pp; English.  
 XX  
 CC The present invention provides a novel fusion polypeptide capable of  
 CC binding a cytokine to form a nonfunctional complex. The invention is  
 CC useful for identifying agonists or antagonists of cytokine receptors and  
 CC for treating cytokine-related diseases or disorders e.g. cancer,  
 CC cachexia, arthritis and osteoporosis. The present sequence is human IL-1  
 CC trap mutant DNA. This mutant construct is obtained by insertion of bases

CC TCCGGA between the position 1077-1078 of the wild type human IL-1 Trap  
CC DNA. Note: This sequence is not shown in the specification, but is  
CC derived from human wild type IL-1 Trap 823 DNA shown as SEQ ID NO: 39  
CC (Acc No: AAD63748) in figure: 41 of the specification  
XX  
SQ Sequence 2709 BP; 822 A; 629 C; 614 G; 644 T; 0 U; 0 Other;

Query Match	48.4%	Score 1043;	DB 10;	Length 2709;
Best Local Similarity	99.5%;	Pred. No. 4.7e-233;		
Matches 1046;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

QY	303	ATGACATTCCTGTCGTGTGTAGTAGTCACTCACTTTATGGAATCCCGCAAAAGTATGCC	362
Db	1	ATGTGCTTCTGTGTGTGTATGTAGTCTCTACTTTTATGGAATCCCGCAAAAGTATGCC	60
QY	363	TCGAAACGCTGCATGACTGTGGGACTAGAACCACTAGAGCAATCCAGTGTGGAAGAT	422
Db	61	TCGAAAGCTGCATGACTGTGGGACTAGAACCACTAGAGCAATCCAGTGTGGAAGAT	120
QY	423	GAGCCAGCTGCATCAAGTGGCCCACTTTTGAAACACTCTGAAATTCATTAAGCACCA	482
Db	121	GAGCCAGCTGCATCAAGTGGCCCACTTTTGAAACACTCTTGAATTCATTAAGCACCA	180
QY	483	GCCCATTCAGCTGGCCTTACTCTGATCTGATTTGACTAGACGAGACCGGACCTTGAG	542
Db	181	GCCCATTCAGCTGGCCTTACTCTGATCTGATTTGACTAGACGAGACCGGACCTTGAG	240
QY	543	GAGCCATTTAACTTCCGCTCCCGGAAACCGCACTTGTATGATAGAGAAAGATGTCTGGG	602
Db	241	GAGCCATTTAACTTCCGCTCCCGGAAACCGCACTTGTATGATAGAGAAAGATGTCTGGG	300
QY	603	TTTCGGCCCACTCTCTCTCAATGACACTGSCACTATACCTGCATGTTAAGGAACATACA	662
Db	301	TTTCGGCCCACTCTCTCTCAATGACACTGSCACTATACCTGCATGTTAAGGAACATACA	360
QY	663	TATTCGACGAAAGTGTGATTTCCCTTGGAAGTTGTTCAAAAGACACCTGTTCATTTCC	722
Db	361	TATTCGACGAAAGTGTGATTTCCCTTGGAAGTTGTTCAAAAGACACCTGTTCATTTCC	420
QY	723	CCCATGAACTCCCACTGACATAAACTGTATATAGAAATATGSCATTCAGAGATCACTGT	782
Db	421	CCCATGAACTCCCACTGACATAAACTGTATATAGAAATATGSCATTCAGAGATCACTGT	480
QY	783	CCAAATGTAGATGATATTTCCCTCCAGTCAAAACCGACTATCACTTGGTATATGGGC	842
Db	481	CCAAATGTAGATGATATTTCCCTCCAGTCAAAACCGACTATCACTTGGTATATGGGC	540
QY	843	TGTTATAAATACAGAAATTTTAAATATGTAATACCCGAAGATATGAACTTGAGTTCTC	902
Db	541	TGTTATAAATACAGAAATTTTAAATATGTAATCCCGAAGATATGAACTTGAGTTCTC	600
QY	903	ATTGCCCTTAATTCGAATAATAGAAATTCACATGTCGTGTTCATATCCAGAAAATGGA	962
Db	601	ATTGCCCTTAATTCGAATAATAGAAATTCACATGTCGTGTTCATATCCAGAAAATGGA	660
QY	963	CGTAGCTTTCATCTCACAGAGCTGTGACTGTAAAGGTATAGGCTCTCCAAAATATGCA	1022
Db	661	CGTAGCTTTCATCTCACAGAGCTGTGACTGTAAAGGTATAGGCTCTCCAAAATATGCA	720
QY	1023	GTGCCCCCTGTATTCATTCACCTAATGATCAGTGTGCTATATAGAAAGAACCGAGAGAG	1082
Db	721	GTGCCCCCTGTATTCATTCACCTAATGATCAGTGTGCTATATAGAAAGAACCGAGAGAG	780
QY	1083	GAGCTACTCATTCCTGTGACGGTCTATTTTATGTTTCTGATGGAATTCGCAATGAGGTT	1142
Db	781	GAGCTACTCATTCCTGTGACGGTCTATTTTATGTTTCTGATGGAATTCGCAATGAGGTT	840
QY	1143	TGGTGGACCAATTGATGGAAGAAAAAAGCTGATGACATCACTATGATGACCAATTAAGAA	1202
Db	841	TGGTGGACCAATTGATGGAAGAAAAAAGCTGATGACATCACTATGATGACCAATTAAGAA	900
QY	1203	AGTATAGCTATAGTAGAAACAGAAAGATGAAACTAGAACTTCAGATTTTGAGCATCAAGAA	1262



Db	901	AGTATAGTCATAGTAGAACAAGATGAACAGAACTCAGATTTTGACATCAAGAA	960
Qy	1263	GTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGTAGAAAGTGCAGGCGAA	1322
Db	961	GTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGTAGAAAGTGCAGGCGAA	1020
Qy	1323	GTGCGAAGCAGCCAGGTGAAGCAGAAAG	1353
Db	1021	GTGCGAAGCAGCCAGGTGAAGCAGAAAG	1051

Search completed: December 25, 2004, 13:17:06  
JOB time : 1041 secs



**This Page Blank (uspio)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using ew model

Run on: December 25, 2004, 12:58:19, Search time 185 Seconds  
(without alignments)  
8279,730 Million cell updates/sec

Title: US-08-917-710-1

Perfect score: 2155  
Sequence: 1 CGGTGGCGCCCTTCTAGAA.....CTAAAAAAAAAAAAAAAAAAAA 2155

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/CTOS.COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1056.8	49.0	1740	3	US-08-991-944-1
2	1043	48.4	2733	4	US-09-313-942-27
3	794.2	36.9	3355	4	US-08-991-944-3
4	133	6.2	229	4	US-09-513-999C-13178
5	102.8	4.6	2061	3	US-09-173-151A-3
6	99.4	4.5	1737	3	US-09-173-151A-1
7	97	4.5	2537	3	US-09-173-151A-34
8	66.8	3.1	2045	3	US-08-793-088A-1
9	62	2.9	1141	4	US-09-806-708B-22
10	61.4	2.8	1141	4	US-09-806-708B-22
11	57.8	2.7	680	4	US-09-489-847-73
12	57.4	2.7	2040	2	US-08-533-669A-5
13	57.4	2.7	2040	3	US-09-183-861-5
14	57.4	2.7	2040	3	US-09-022-765-5
15	57.4	2.7	2040	4	US-09-551-974A-5
16	57.4	2.7	2040	4	US-09-565-501A-5
17	57.4	2.7	2040	4	US-09-639-206A-5
18	57.4	2.7	2040	4	US-09-874-923-5
19	57.4	2.7	2040	4	US-08-798-841-5
20	57	2.6	1850	3	US-08-617-860B-32
21	57	2.6	4088	2	US-08-605-106-4
22	56.2	2.6	3089	1	US-08-472-934-5
23	56.2	2.6	3089	2	US-08-323-460A-5
24	56.2	2.6	3089	2	US-08-461-146C-5
25	56.2	2.6	3089	3	US-08-461-146C-5
26	56.2	2.6	3089	3	US-08-628-823-9
27	55.4	2.6	1774	4	US-09-489-847-17

28	55.4	2.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
29	55.2	2.6	867	4	US-09-204-865-8	Sequence 8, Appl
30	55	2.6	500	3	US-08-818-112-101	Sequence 101, App
31	55	2.6	500	3	US-08-818-111-96	Sequence 96, Appl
32	55	2.6	500	3	US-09-056-556-101	Sequence 101, App
33	55	2.6	500	4	US-09-072-596-96	Sequence 96, Appl
34	55	2.6	500	4	US-09-072-967-101	Sequence 101, Appl
35	55	2.6	506	3	US-09-227-357-116	Sequence 116, App
36	55	2.6	860	3	US-08-998-416-287	Sequence 287, App
37	54.4	2.5	1542	4	US-09-345-473E-13	Sequence 13, Appl
38	54.2	2.5	1378	1	US-08-075-533-20	Sequence 20, Appl
39	54.2	2.5	1378	2	US-08-948-176-20	Sequence 20, Appl
40	54.2	2.5	1378	5	PCT-US91-09160-20	Sequence 20, Appl
41	54.2	2.5	1517	4	US-09-904-615-64	Sequence 64, Appl
42	54.2	2.5	3300	4	US-09-482-273-68	Sequence 68, Appl
43	54.2	2.5	4062	4	US-09-270-767-5814	Sequence 5814, Ap
44	54.2	2.5	4062	4	US-09-270-767-21096	Sequence 21096, A
45	54	2.5	1463	4	US-09-501-115-3	Sequence 3, Appl

## ALIGNMENTS

```
RESULT 1
US-08-991-944-1
; Sequence 1, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
; TITLE OF INVENTION: Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,944
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1719
; US-08-991-944-1
;
Query Match 49.0%; Score 1056.8; DB 3; Length 1740;
Best local similarity 99.8%; Pred. No. 4.7e-283;
Matches 1059; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
294 TCTCAAGAGTACCTTCTGTGTGTAGTAGTCTACTTTATGGAATCCCGCA 353
```

[illegible]

```

? Sequence 27, Application US/09313942
? Patent No. 6472179
? GENERAL INFORMATION:
? APPLICANT: REGENERON PHARMACEUTICALS, INC.
? TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
? TITLE OF INVENTION: AND USING
? FILE REFERENCE: REG 203-A
? CURRENT APPLICATION NUMBER: US/09/313,942
? CURRENT FILING DATE: 1999-05-19
? PRIOR APPLICATION NUMBER: 09/313,942
? PRIOR FILING DATE: 1999-05-19
? PRIOR APPLICATION NUMBER: 60/101,858
? PRIOR FILING DATE: 1998-09-25
? NUMBER OF SEQ. ID NOS: 32
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ. ID NO 27
? LENGTH: 2733
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(2730)
? US-09-313-942-27

```

	Query Match	Similarity	48.4%	Score 1043	DB 4	Length 2733	
	Best Local	Similarity	99.5%	Pred. No.	4-2e-279		
	Matches 1046	Conservative	0	Mismatches	5	Indels	Gaps 0
QY	303	ATGACACTTCTGTGSGTGTGTAGTGAAGTCTCTACTTTTATGTGAATCTCTGCAAACTGATGCC	362				
DB	1	ATGTGCTCTCTGTGTGTGTGTAGTGAAGTCTCTACTTTTATGTGAATCTCTGCAAAAGTGAAGCC	60				
QY	363	TCGAAAGCGTCGCAATGACTGGGGACTGAGCAACCATGAGGCAAAATCTCAAGTGTTTGAAGAT	422				
DB	61	TCGAAAGCGTCGCAATGACTGGGGACTGAGCAACCATGAGGCAAAATCTCAAGTGTTTGAAGAT	120				
QY	423	GAGCCAGCTCGCATCAAGTGTCCCACTCTTTGAACAATTCTTGAAATTCATACAGACA	482				
DB	121	GAGCCAGCTCGCATCAAGTGTCCCACTCTTTGAACAATTCTTGAAATTCATACAGACA	180				
QY	483	GCCCATTCAGTGGGCTTACTCTGATCTGATTTGGACTGAACGCGGACCTTGAG	542				
DB	181	GCCCATTCAGTGGGCTTACTCTGATCTGATTTGGACTGAACGCGGACCTTGAG	240				
QY	543	GAGCCCAATTAATTCCGCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGTCTGTG	602				
DB	241	GAGCCCAATTAATTCCGCTCCCGAGAACCGCATTTAGTAAGAGAAAGATGTCTGTG	300				
QY	603	TTCCGGGCCCACTCTCTCAATGACACGTGGCACTATACCTGCACTGAAGGAACACTACA	662				
DB	301	TTCCGGGCCCACTCTCTCAATGACACGTGGCACTATACCTGCACTGAAGGAACACTACA	360				
QY	663	TATTCAGCAAAAGTTGCATTTTCCCTTGGAACTGTTCAAAAAGACAGTGTTCATTTCC	722				
DB	361	TATTCAGCAAAAGTTGCATTTTCCCTTGGAACTGTTCAAAAAGACAGTGTTCATTTCC	420				
QY	723	CCCATGAACCTCCAGTGCATAAACGTGATATAGAAATATGGCACTTCAGAGATCACTGT	782				
DB	421	CCCATGAACCTCCAGTGCATAAACGTGATATAGAAATATGGCACTTCAGAGATCACTGT	480				
QY	783	CCAAATGTAGATGATATTTCTCTCCAGTGTCAAAACCGACTATCACTGTGTATATGSGC	842				
DB	481	CCAAATGTAGATGATATTTCTCTCCAGTGTCAAAACCGACTATCACTGTGTATATGSGC	540				
QY	843	TGTTTAAATATACGAATTTTAAATATATGTATACCCGAAGTATGAACTTGAAGTTCTC	902				
DB	541	TGTTTAAATATACGAATTTTAAATATATGTATACCCGAAGTATGAACTTGAAGTTCTC	600				
QY	903	ATTGCGTTAATTTCCAAATATGAAATTAACAATGTGTGTTAACATATCCGAATAATGA	962				
DB	601	ATTGCGTTAATTTCCAAATATGAAATTAACAATGTGTGTTAACATATCCGAATAATGA	660				
QY	963	CGTAGCTTACTCTACACGAGACTCTGACTTAAGATAGAGCTTCCAAAAAATATGA	1022				



Db 1151 GGAAGCTGAGCAGCTGCCAAGTGTAACAGAAAG 1185

RESULT 4  
US-09-513-999C-13178  
Sequence 13178, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59, US2, REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 3681  
SOFTWARE: Patent.pm  
SEQ ID NO: 13178  
LENGTH: 229  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-13178

Query Match 6.2%; Score 133; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3,8e-27;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 TCACTGGGGAGAGCTGCCGGATCCAGGCTTCGCCGGGTCCTTTGGCCAGAGGCCCGGA 141  
Db 1 TCACTGGGGAGAGCTGCCGGATCCAGGCTTCGCCGGGTCCTTTGGCCAGAGGCCCGGA 60

QY 142 AGAAGAGAGTGGCCGGCGACACTGACACCCATCCCGGCGCTTTTGGCGGCGCTCTAGC 201  
Db 61 AGAAGAGAGTGGCCGGCGACACTGACACCCATCCCGGCGCTTTTGGCGGCGCTCTAGC 120

QY 202 TTCCCAAGAAAG 214  
Db 121 TTCCCAAGAAAG 133

RESULT 5  
US-09-173-151A-3  
Sequence 3, Application US/09173151A  
Patent No. 6326472  
GENERAL INFORMATION:  
APPLICANT: Timans, Jacqueline C.  
APPLICANT: Debets, Johannes Eduard Maria  
APPLICANT: Antonius  
APPLICANT: Sana, Theodore R.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: DMAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/173,151A  
FILING DATE: 14-OCT-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/065,776  
FILING DATE: 17-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/078,008  
FILING DATE: 12-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/081,883  
FILING DATE: 15-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/095,987  
FILING DATE: 10-AUG-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/078,416  
FILING DATE: 18-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/062,066  
FILING DATE: 15-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0767X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2061 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2058  
US-09-173-151A-3

Query Match 4.8%; Score 102.8; DB 3; Length 2061;  
Best Local Similarity 50.9%; Pred. No. 3.5e-18;  
Matches 329; Conservative 0; Mismatches 302; Indels 15; Gaps 3;

QY 313 TGTGTGTGTAGTGAAGTCTCTTCTTATGATCTCTGCAAGATGCTGCTGAGACGCT 372  
Db 32 TGTGTGTGTAGTGAAGTCTCTTCTTATGATCTCTGCAAGATGCTGCTGAGATGCT 91

QY 373 GCGATGACTGGGAGCTAGACACCCATGAGGCAATCCAGTGTGTAAGTACCGACGTC 432  
Db 92 GCGATGACTGGGAGCTAGACACCCATGAGGCAATCCAGTGTGTAAGTACCGACGTC 148

QY 433 GATCAAGGCCACCTTTTGAACACTTCTTGAATTCACCTACAGCAGCCCAATTGAG 492  
Db 149 GATCAAGGCCACCTTTTGAACACTTCTTGAATTCACCTACAGCAGCCCAATTGAG 208

QY 493 CTGGCCTTACTGATCTGTATTTGGACTAGACAGGACCGGACCTTGAGACCAATTA 552  
Db 209 CTGGCCTTACTGATCTGTATTTGGACTAGACAGGACCGGACCTTGAGACCAATTA 262

QY 553 ACTTCGGCTCCCGGAGAACCGCATTAAGAGAAAGATGCTGTGTCGGGCCCA 612  
Db 263 TCTTTT-----CAGAGGTGAGATGAGCAAGAGAAATTCATATGTTTCACTAG 316

QY 613 CTCTCTCATGACACTGCACTATATACCTGATGTTTGAAGACATACATATTCAGCA 672  
Db 317 CTGAGGACAAAGACATGATTCATACCTGTTTGAAGACATACATATTCAGCA 376

QY 673 AAGTTCATTTCCCTTGAAGTGTTCAAAAGACAGCTGTTCAATTCCTCCATGAAG 732  
Db 377 AAGTTCATTTCCCTTGAAGTGTTCAAAAGACAGCTGTTGCTCAACAGCAGGA 436

QY 733 TCCAGATGATAGATGATATGATATGATGATGATGATGATGATGATGATGATGATG 792  
Db 437 TCCGCTATTGAAATATCTGAAGTACCTAAAGAAAGAGATCTCTCTCCAGCATGG 496

QY 793 ATGATATTTTCTTCCAGTGTCAACGACATATCACTTGATATGAGGCTGTATATAA 852



QY 906 GCGTAAATTCATATGAAATTCACATGTTGTTACATATCCAGAAA 958  
 Db 595 GTTCAAGAGAGATGAGAGAAATTCACATGTTGTTAAATATGAGGAAA 647

RESULT 7  
 US-09-173-151A-34  
 / Sequence 34, Application US/09173151A  
 / Patent No. 6326472  
 / GENERAL INFORMATION:  
 / APPLICANT: Timans, Jacqueline C.  
 / APPLICANT: Debets, Johannes Eduard Maria  
 / APPLICANT: Antonius  
 / APPLICANT: Sana, Theodore R.  
 / APPLICANT: Bazan, J. Fernando  
 / APPLICANT: Kastelein, Robert A.  
 / TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods  
 / NUMBER OF SEQUENCES: 36  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: DNAX Research Institute  
 / STREET: 901 California Avenue  
 / CITY: Palo Alto  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94304-1104  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/173,151A  
 / FILING DATE: 14-OCT-1998  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/065,776  
 / FILING DATE: 17-NOV-1997  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/078,008  
 / FILING DATE: 12-MAR-1998  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/081,883  
 / FILING DATE: 15-APR-1998  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/095,987  
 / FILING DATE: 10-AUG-1998  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/078,416  
 / FILING DATE: 18-MAR-1998  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/062,066  
 / FILING DATE: 15-OCT-1997  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: CHING, Edwin P.  
 / REGISTRATION NUMBER: 34,090  
 / REFERENCE/DOCKET NUMBER: DX0767X  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (650)852-9196  
 / TELEFAX: (650)496-1200  
 / INFORMATION FOR SEQ. ID NO.: 34:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 2537 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: cDNA  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 1..2004  
 / US-09-173-151A-34

Query Match

4.5%; Score 97; DB 3; Length 2537;

Best Local Similarity 49.7%; Pred. No. 1.6e-16;  
 Matches 278; Conservative 0; Mismatches 275; Indels 6; Gaps 1;  
 QY 396 ATGAGCAATTCAGAGTGTGTTGAAGATGAGCCAGCTCCGATTAAGTCCCACTCTTGA 455  
 Db 28 ATCAAGAAATATCAAGTTTGTGGAGAGCCCTGTCATTAATGAGCACTCTTTAT 87  
 QY 456 CACTTCTGAATTAATCACTACAGCAAGCCCAATTCAGCTGCGCTTACTCTGATCTGAT 515  
 Db 88 GGTATATACAGAAATTAATTCCTCCCTGCGCAAAAGTGTGATGATGATGATGATGAT 147  
 QY 516 TGGACTAGCAGAGACCGGAGCTTGAAGAGCCCAATTAATTCCTGCGCTCCCGAGACCG 575  
 Db 148 AAAAGTTCTGCTCTGAGACCTTGAAGAGCCCAATGAGCT-----TTGACGGAATGAG 201  
 QY 576 ATTAGTAAGAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 635  
 Db 202 ATGAGCAAGAGAAATCAATTCATTTGTTGCGGCAACTTCTACAGAGAGTGTCTC 261  
 QY 636 TATACCTGATGTTAAGAACATCAATATGACAGCAAAATTCATTTCTTGAAGTT 695  
 Db 262 TAGCCTGTGATAGAGATCACTCACTTACTGTATGAAGATTCATCTCAGTACAGTG 321  
 QY 696 GTTCAAAAAGACAGCTGTTCAATTCGCCCAATGAAGTCCGATGATTAATGATTA 755  
 Db 322 GGTGAAAATGACACTGAGCTGCTAATTAATTCAGATGATTAATTTGAAAAAGCTGA 381  
 QY 756 GAATATGCAATTCAGAGATCACTGTCCTCAATGATGATTAATTTCTTCAAGTGC 815  
 Db 382 CTAGCAAAAGCAAGAAATTTCAATGCGGTGATAGAGATTTCTACGCAACAGA 441  
 QY 816 AAACGACTATCATCTGTATATGCGCTGTATTAATACAGAAATTTAATATGATTA 875  
 Db 442 GAACCTGAATCTCTTGTACAGAGATGACAGCAAAACATGAGGCAAGTATGTA 501  
 QY 876 CCGAGATGATGAGCTGATGTTCCCATGCTTATTTCAATTAATGAAATATACAGA 935  
 Db 502 TTAAAAAGATATCTTCTTATAGAGAGATGAGAGAGATGAGAGATGAGATTAATACC 561  
 QY 936 TGTGTTTACATATCCAG 954  
 Db 562 TGTGAATTAATATGAG 580

RESULT 8  
 US-08-795-088A-1  
 / Sequence 1, Application US/08795088A  
 / Patent No. 6242569  
 / GENERAL INFORMATION:  
 / APPLICANT: Sul, Hong-Bing  
 / APPLICANT: Goeddel, David V.  
 / TITLE OF INVENTION: Regulators of Apoptosis  
 / NUMBER OF SEQUENCES: 3  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Science & Technology Law Group  
 / STREET: 75 Denise Drive  
 / CITY: Hillsborough  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94010  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/795,088A  
 / FILING DATE:  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Osman, Richard A.  
 / REGISTRATION NUMBER: 36,627  
 / REFERENCE/DOCKET NUMBER: T97-001





Oy 683 TCCCTGGAGGTTCTTCAAAGAAGCAGGTGTTTCAATTCGCCCAATGAAATCCAGCA 742  
 Db 184 WNNNGCEVTVMVVYKTKDRODSBEMVYGMWVKNWSIDVTVYVWVMDMKRYRVR 243  
 Oy 743 TAAACTGTATATAGAAATATGSCATTTCAGAGATCACTTGTCCAAATGTAGATGATTT 802  
 Db 244 TRGRMNVMVMBVTAHRRRYNNNGVTEBAVYRRMTNNNNNNNAKMKRAKXWGMRAV 303  
 Oy 803 TCCCTCCAGTGTCAAACCGACTATCACTGGTATATGCGCTGTTATATAAATACGAATTT 862  
 Db 304 STCTTWSKTTKVTSTCVANNCRAGDANKDHKKMSAAWVYNNNNNNWYTKARHB 363  
 Oy 863 TAAATGTATAACCCGAGGTATGAATCTG--AGTTTCCATTCGCTTAATTTCAAT 920  
 Db 364 ARMDVMVHSARKWHAANAAYSRKKWTEYKKTWNNNGTITWKRMAWYKMDMDWG 423  
 Oy 921 AATGGAATTCACATGTGTTGTTACATATTCAGAAAATGACGATGCTTCACTCAC 980  
 Db 424 TYNNNNNGRTTYTWTNKKKMTTYKYVANNCKPAMDHKTCHNTNTTWWCKTYNNCY 483  
 Oy 981 AGACCTCGACTGATAAGGTAGTGGCTCTCAAAAATGACAGTCCCTGTATCAT 1040  
 Db 484 WKSMTNGSHBAAAVTVYVWVNNRRYVHANNMMWDYWKACTYKTVKVBVCSKMMNVYAAW 543  
 Oy 1041 TCACCTAATGATCATGTGCTGTATGAGAAAGACGAGAGAGACTATCTATTCCTGT 1100  
 Db 544 YTKSMVNTSRYYRWKTKTNSWRKRSDETSMRANNVYAABHYGYKMTIRWMBSHTBHB 603  
 Oy 1101 ACGCTATATTTAGTTTTCGATGAGTCTCGCAATAGAGTGTGGTGACAT-----TG 1155  
 Db 604 RAGAAHWEEMVYBKCHCMQAKWYKAKKYAAGSGSNNNNNNNNNNNNNNNNATCAEDDY 663  
 Oy 1156 ATGAAAAAAACCTGATGACATCACTATTGATGTCACCATTAAGAAAGTATTAAGTCATA 1215  
 Db 664 AASRVYMANAKWYVYKAAANNAAYYTHANNWGCNNATDPRITWKKNNNNNAGTWKN 723  
 Oy 1216 GTAGAACGAGATGAACCTGAATCTGATTTTGAGCATGAAGAAAGTTACCTGTAGG 1275  
 Db 724 NNNNAKVASAKNPAAAVKAKKHWRANVAFMGADAAABTTDPRNGAYTKYTTT 783  
 Oy 1276 ATCTCAAGCGCAGTATGCTGTGATGCTAGAGTCCCAAGGCGAAAGTTGCCAAAGCAG 1335  
 Db 784 NNNNTYGVVYNTAPADGMANNNNNNNNNNNNNNNNNGMSDMWYTWVAAYVGINNNNNNN 843  
 Oy 1336 CCAAGGTGAGCAGAAAGTATATGATGCGGTGAGTATGAATCTCTGAGTCCAAATTA 1395  
 Db 844 NAYAMVMTWKMYTTTDDRWBRBAYTNNNNNNRFAAYGAYDDAAYYMSDTCDAWMDATKM 903  
 Oy 1396 ACATTTGGTGAATPAAGACAAAAGAGAGATTGAGAACAGAGAGCTCCAGACCTGAGC 1455  
 Db 904 NNATTTNRGVIMRTNN 963  
 Oy 1456 CTGACGCGACTTAACCCATAGTAAATGAATCAAACTTAATGAAAAATATGAAGTTTCA 1515  
 Db 964 WNNCTTTCRKXKNNCTWYTWMTTTRTTTYAATPRKTNATGSMTRCATGKNNNNYWTGW 1023  
 Oy 1516 TCTATGTAGATACCTCAAAATATGTGTTCTGTATATGTTA 1555  
 Db 1024 KTRWTVAYMATRMMKAMWKVATGSMNTNSYARMAVYKTPA 1063  
 RESULT 11  
 US-09-489-847-73  
 ; Sequence 73, Application US/09489847  
 ; Patent No. 6476195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al  
 ; TITLE OF INVENTION: 98 Human Secretd Proteins  
 ; FILE REFERENCE: P2031p1  
 ; CURRENT APPLICATION NUMBER: US/09/489,847  
 ; CURRENT FILING DATE: 2000-01-24  
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130  
 ; EARLIER FILING DATE: 1999-07-29

```

? EARLIER APPLICATION NUMBER: 60/094,657
? EARLIER FILING DATE: 1998-07-30
? EARLIER APPLICATION NUMBER: 60/095,486
? EARLIER FILING DATE: 1998-08-05
? EARLIER APPLICATION NUMBER: 60/096,319
? EARLIER FILING DATE: 1998-08-12
? EARLIER APPLICATION NUMBER: 60/095,454
? EARLIER FILING DATE: 1998-08-06
? EARLIER APPLICATION NUMBER: 60/095,455
? EARLIER FILING DATE: 1998-08-06
? NUMBER OF SEQ. ID NOS: 376
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 73
? LENGTH: 680
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (7)
? OTHER INFORMATION: n equals a,t,g, or c
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (9)
? OTHER INFORMATION: n equals a,t,g, or c
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (15)
? OTHER INFORMATION: n equals a,t,g, or c
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (16)
? OTHER INFORMATION: n equals a,t,g, or c
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (22)
? OTHER INFORMATION: n equals a,t,g, or c
US-03-489-847-73

Query Match      2.7%; Score 57.8; DB 4; Length 680;
Best Local Similarity 80.0%; Pred. No. 5.5e-06;
Matches 68; Conservative 0; Mismatches 17; Indels 0; Gaps 0

Qy      1 CGGTGGCGCCCGTTCTAGACTAGTGTATCCCGGGATCGAGAAATTCGGCAGAGAAA 60
Db      33 CGGTGGCGCCCGCTCTAGACTAGTGTATCCCGGGCTCAGAGAAATTCGGCAGAGATA 92

Qy      61 GTCCGGCGGAAAGTAAAGCCTCAC 85
Db      93 TTTCGCTGAGCCCTAGAAAAGCCAC 117

RESULT 12
US-08-533-669A-5
? Sequence 5, Application US/08533669A
? Patent No. 5834592
? GENERAL INFORMATION:
? APPLICANT: Corixa Corporation
? TITLE OF INVENTION: LETHMANIA ANTIGENS FOR USE IN THE
? TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LETHMANIASIS
? NUMBER OF SEQUENCES: 18
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SEED AND BERRY LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? City: Seattle
? STATE: Washington
? COUNTRY: USA
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/533,669A  
FILING DATE: 22-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.420  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2040 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 62..2029  
US-08-533-669A-5

Query Match  
Best Local Similarity 76.9%; Score 57.4; DB 2; Length 2040;  
Pred. No. 1.4e-05;  
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CGGTGGCGCCCGCTTCTAGAACTAGTGCATCCCGGGATGCAGAAATTCGGCAGAGAA 60  
DB 3 CGGTGGCGCCCGCTTCTAGAACTAGTGCATCCCGGGATGCAGAAATTCGGCAGAGAA 62

QY 61 GTGCGCGCGGAAAGTAAGAGCTCACTGGGGA 91  
DB 63 GCCTGACGACCCGCGCGTGTCTGGCGGAGGA 93

RESULT 13  
US-09-183-861-5  
Sequence 5, Application US/09183861  
Patent No. 6355165  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Campos-Neto, Antonio  
APPLICANT: Webb, John R.  
APPLICANT: Dillon, David C.  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/183,861  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/022,765  
FILING DATE: 12-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.420C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2040 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 62..2029  
US-09-022-765-5

SEQUENCE CHARACTERISTICS:  
LENGTH: 2040 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 62...2029  
US-09-183-861-5

Query Match  
Best Local Similarity 76.9%; Score 57.4; DB 3; Length 2040;  
Pred. No. 1.4e-05;  
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CGGTGGCGCCCGCTTCTAGAACTAGTGCATCCCGGGATGCAGAAATTCGGCAGAGAA 60  
DB 3 CGGTGGCGCCCGCTTCTAGAACTAGTGCATCCCGGGATGCAGAAATTCGGCAGAGAA 62

QY 61 GTGCGCGCGGAAAGTAAGAGCTCACTGGGGA 91  
DB 63 GCCTGACGACCCGCGCGTGTCTGGCGGAGGA 93

RESULT 14  
US-09-022-765-5  
Sequence 5, Application US/09022765  
Patent No. 6375955  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Campos-Neto, Antonio  
APPLICANT: Webb, John R.  
APPLICANT: Dillon, David C.  
APPLICANT: Skeiky, Yasir A.W.  
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,765  
FILING DATE: 12-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.420C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2040 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 62..2029  
US-09-022-765-5

Query Match  
Best Local Similarity 76.9%; Score 57.4; DB 3; Length 2040;  
Pred. No. 1.4e-05;  
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY      1  CCGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGATGCAGAAATTCGGACGAGAA 60
      |||
Db      3  CCGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGCTGCAGAAATTCGGACGAGAA 62
      |||

QY      61  GTCCGGCGGAGTAAGAGCTCACTGGGGA 91
      |||
Db      63  GCCTGACGAGCCCGGCGGTCTGGGCGAGGA 93
      |||
```

## RESULT 15

```
US-09-551-974A-5
; Sequence 5, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420CS
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Leishmania braziliensis
US-09-551-974A-5
```

```
Query Match      2.7%; Score 57.4; DB 4; Length 2040;
Best Local Similarity 76.9%; Pred. No. 1.4e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

```
QY      1  CCGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGATGCAGAAATTCGGACGAGAA 60
      |||
Db      3  CCGTGGCCGCCGTTCTAGACTAGTGCATCCCCCGGCTGCAGAAATTCGGACGAGAA 62
      |||

QY      61  GTCCGGCGGAGTAAGAGCTCACTGGGGA 91
      |||
Db      63  GCCTGACGAGCCCGGCGGTCTGGGCGAGGA 93
      |||
```

Search completed: December 25, 2004, 17:43:38  
Job time : 189 secs



Db	121	ATGCTATGTGATCATCAGCTTAGAAGCTGAGAGGCTC-TAGAGCTGCATCTC	179
Qy	276	TTGCCCCCTCCCTTATATCTGCAAGAGTGCACCTTCGTGGTGTGTAAGTCTTCAC	335
Db	180	TTGCCCTCCCTTTATATCTCAAGAGTGCACCTTCGTGGTGTGTAAGTCTTCAC	239
Qy	336	TTTTATAGAACTCCTGCAAGAGTGCAGGCTGCAGTACATGACGAGGAGCTAGACAC	395
Db	240	TTTTATAGAACTCCTGCAAGAGTGCAGGCTGCAGTACATGACGAGGAGCTAGACAC	299
Qy	396	ATGAGCAATCCAGTGTGTAAGATAGCAGCTGCATCAAGTCCCACTCTTGGAA	455
Db	300	ATGAGCAATCCAGTGTGTAAGATAGGCACTGCATCAAGTCCCACTCTTGGAA	359
Qy	456	CACCTTCTGAATTCATCTACAGCACAGCCCATTCAGCTGGCTTACTGTGATCTGTAT	515
Db	360	CACCTTCTGAATTCATCTACAGCACAGCCCATTCAGCTGGCTTACTGTGATCTGTAT	419
Qy	516	TGACATACAGAGACCGGAGCTTGAAGAGCCATTTAACTCCGCTCCCGAGAAACGC	575
Db	420	TGACATACAGAGACCGGAGCTTGAAGAGCCATTTAACTCCGCTCCCGAGAAACGC	479
Qy	576	ATTAGTAGAGAGAAAGATGTGCTGTGGTTCGGGCCCATCTCTCTCAATGACATGCAAC	635
Db	480	ATTAGTAGAGAGAAAGATGTGCTGTGGTTCGGGCCCATCTCTCTCAATGACATGCAAC	539
Qy	636	TATACCTGATGTTAAGGAACCTACATATGAGCAGCAAGTGCATTTCCCTTGGAGAT	695
Db	540	TATACCTGATGTTAAGGAACCTACATATGAGCAGCAAGTGCATTTCCCTTGGAGAT	599
Qy	696	GTTCAAAAAGACAGCTGTTTCAATTCGCCCATGAACTCCAGTGCATAACTGTATATA	755
Db	600	GTTCAAAAAGACAGCTGTTTCAATTCGCCCATGAACTCCAGTGCATAACTGTATATA	659
Qy	756	GATATGAGATCAGAGATCATCTTGCCAAATGTATAGATTTTCCCTCCAGTGC	815
Db	660	GATATGAGATCAGAGATCATCTTGCCAAATGTATAGATTTTCCCTCCAGTGC	719
Qy	816	AAACCCACTCATCTTGGTATATGGCGGTATATAAATATAGATTTTATATGTATATA	875
Db	720	AAACCCACTCATCTTGGTATATGGCGGTATATATAAATATAGATTTTATATGTATATA	779
Qy	876	CCGGAAGTATGAACTTGATTTCTCATTCGCTTAAATTCAAATATGGAATTTACACA	935
Db	780	CCGGAAGTATGAACTTGATTTCTCATTCGCTTAAATTCAAATATGGAATTTACACA	839
Qy	936	TGTGTTGTTACATATCCAGAAATATGAGTGCAGTTTATCTACACAGACTGCACTGTA	995
Db	840	TGTGTTGTTACATATCCAGAAATATGAGTGCAGTTTATCTACACAGACTGCACTGTA	899
Qy	996	AACGATAGAGCTTCCAAAATATGACGTGCCCTGTGATCCATTCACCTAATGATCAT	1055
Db	900	AACGATAGAGCTTCCAAAATATGACGTGCCCTGTGATCCATTCACCTAATGATCAT	959
Qy	1056	GTCGCTATAGAAAGAACCCAGAGAGAGTACTCATTCCTGTAAGGCTATTTTGGT	1115
Db	960	GTCGCTATAGAAAGAACCCAGAGAGAGTACTCATTCCTGTAAGGCTATTTTGGT	1015
Qy	1116	TTTCTGATGATTTCTGCAATGAGGTTTGTGACCAATTGAGAAAAAAACCTGATGAC	1175
Db	1020	TTTCTGATGATTTCTGCAATGAGGTTTGTGACCAATTGAGAAAAAAACCTGATGAC	1075
Qy	1176	ATACATATATGATGTCAACCTTTACGAAGATATAGTATAGTATGAAACAGAAATGAAAT	1233
Db	1080	ATACATATATGATGTCAACCTTTACGAAGATATAGTATAGTATGAAACAGAAATGAAAT	1133
Qy	1236	AGAACTCAGATTTTGAAGCATCAAGAAATTTACTCTGAGATCTCAAGGCGAGCTATGTC	1295
Db	1140	AGAACTCAGATTTTGAAGCATCAAGAAATTTACTCTGAGATCTCAAGGCGAGCTATGTC	1195
Qy	1296	TGTCATGCTAGAAAGTGCCAAAGGCGAATTTGCCAAAGCAGCAAGGTGAAGCAGAAAG	1353

DB	1200	TCGCATGCTAGAAAGTCCCAAGGCGCAAGTGTCCCAAGAGCCCAAGTGAAGCAGAAAG	1257
RESULT 2			
US-10-717-597-14			
Sequence 14, Application US/10717597			
Publication No. US20040110221A1			
GENERAL INFORMATION:			
APPLICANT: Wyeth			
APPLICANT: Birczynski, Michael E.			
APPLICANT: Twine, Natalie C.			
APPLICANT: Dornier, Andrew J.			
APPLICANT: Trepicchio, William L.			
APPLICANT: Slonim, Donna K.			
APPLICANT: Stover, Jennifer A.			
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS			
FILE REFERENCE: AM101080L			
CURRENT APPLICATION NUMBER: US/10/717,597			
PRIOR FILING DATE: 2003-11-21			
PRIOR APPLICATION NUMBER: US 60/459,782			
PRIOR FILING DATE: 2003-04-03			
PRIOR APPLICATION NUMBER: US 60/427,982			
PRIOR FILING DATE: 2002-11-21			
NUMBER OF SEQ ID NOS: 4904			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 14			
LENGTH: 4724			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-717-597-14			
Query Match	57.7%;	Score 1242.8;	DB 17; Length 4724;
Best Local Similarity	99.8%;	Pred. No. 7.1e-258;	
Matches 1255; Conservative	0;	Mismatches 2;	Indels 1; Gaps 1
QY	96	TGCGGGAGATCCAGGTCCTCCGGGGTCCGCTTTGGCCAGAGGGCGCGAAGAGAGTGGCC	155
DB	1	TGCGGGAGATCCAGGTCCTCCGGGGTCCGCTTTGGCCAGAGGGCGCGAAGAGAGTGGCC	60
QY	156	GCGGACATGACCCCATCCCGGCTGCTTTGCTCTCGCCCTCTAGCTTCCCAAGAAAGC	215
DB	61	GCGGACATGACCCCATCCCGGCTGCTTTGCTCTCGCCCTCTAGCTTCCCAAGAAAGC	120
QY	216	ATGCTATGTGATCATCCCTPAAGACATGAAACATGACAGGGCCCTTAGAAGCTCACTC	275
DB	121	ATGCTATGTGATCATCCCTPAAGACATGAAACATGACAGGGCCCTTAGAAGCTCACTC	179
QY	276	TTGCCCCCTCCCTTTATATCTCAAGAGTGAACCTTCGTGTGTGTAGTGACTCTTAC	335
DB	180	TTGCCCCCTCCCTTTATATCTCAAGAGTGAACCTTCGTGTGTGTAGTGACTCTTAC	239
QY	336	TTTTATGGAATCTCTGCAAGTGTATGCTCTCAAGCGCTGCGATGACTGTGGGACATGACAC	395
DB	240	TTTTATGGAATCTCTGCAAGTGTATGCTCTCAAGCGCTGCGATGACTGTGGGACATGACAC	299
QY	396	ATAGGCAATCCCAAGTGTGTTAAGATGAGCGACCTGCGATCAAGTGTCCACTCTTTGAA	455
DB	300	ATAGGCAATCCCAAGTGTGTTAAGATGAGCGACCTGCGATCAAGTGTCCACTCTTTGAA	359
QY	456	CACCTTGTGAAATTCACACTACGACGACGCCCATTCAGCTGAGCTTACTCTGATCTGTAT	515
DB	360	CACCTTGTGAAATTCACACTACGACGACGCCCATTCAGCTGAGCTTACTCTGATCTGTAT	419
QY	516	TGAGCAACAGAGACCGGGACCTTGAGAGCGCAATTAATTCGCGCTCCGCCGAGAACCG	575
DB	420	TGAGCAACAGAGACCGGGACCTTGAGAGCGCAATTAATTCGCGCTCCGCCGAGAACCG	479
QY	576	ATTAGTAGAGAGAAAGATGTGCTGTGTGTTCGCGCCACTCTCTCAATGACACTGTGAAC	635
DB	480	ATTAGTAGAGAGAAAGATGTGCTGTGTGTTCGCGCCACTCTCTCAATGACACTGTGAAC	539
QY	636	TAACTCTGATGTTAAGAACATCAATTGAGGCAAGTGTGATTTCCCTTGGAAAGTT	695

Db	540	TATACCTGCATGTTAAGAAACACTACATATGTCAGCAAAAGTTGCAATTTCCCTTGAAAGTT	599
Qy	696	GTTCAAAAAGACAGCGTCTTTCAATTTCCCCAGAAACCTCCAGTGCATAAATCTGATATA	755
Db	600	GTTCAAAAAGACAGCGTCTTTCAATTTCCCCAGAAACCTCCAGTGCATAAATCTGATATA	659
Qy	756	GAATATGCAATTAGAGGATCACTTGTCAAATGATAGATATATTTCCCTCCAGTGC	815
Db	660	GAATATGCAATTAGAGGATCACTTGTCAAATGATAGATATATTTCCCTCCAGTGC	719
Qy	816	AAACCGACTATCACTTGATATATGGGCTGTATAAATATACGAATTTTAATATGTAATA	875
Db	720	AAACCGACTATCACTTGATATATGGGCTGTATAAATATACGAATTTTAATATGTAATA	779
Qy	876	CCGGAAGGTATGAACCTGAGTTCCGATCGCATATTTGCAATTAATGGAATTTACACA	935
Db	780	CCGGAAGGTATGAACCTGAGTTCCGATCGCATATTTGCAATTAATGGAATTTACACA	839
Qy	936	TGTGTGTGTTACATATCCAGAAAAATGACGTACGTTTCACTCACAGACCTGACTGTA	995
Db	840	TGTGTGTGTTACATATCCAGAAAAATGACGTACGTTTCACTCACAGACCTGACTGTA	899
Qy	996	AAGGTACTAGCTCTCCAAAAATGAGAGCCCCCTGATGCCATTCACTTAATGATCAT	105
Db	900	AAGGTACTAGCTCTCCAAAAATGAGAGCCCCCTGATGCCATTCACTTAATGATCAT	959
Qy	1056	GTGGTCTATAGAAAGAACCCAGAGAGGAGTACTCATTTCCCTTACGGTCTATTTTAGT	1111
Db	960	GTGGTCTATAGAAAGAACCCAGAGAGGAGTACTCATTTCCCTTACGGTCTATTTTAGT	1011
Qy	1116	TTTCTGATGGAATCTCGCAATGAAGTTTGCTGACCATTTGATGAAAAAAACCTGATGAC	1177
Db	1020	TTTCTGATGGAATCTCGCAATGAAGTTTGCTGACCATTTGATGAAAAAAACCTGATGAC	1077
Qy	1176	ATCACTATTGATGTACCAATTAACGAAAGATATTAATCACTATAGAAACGAAAGTGAACCT	1233
Db	1080	ATCACTATTGATGTACCAATTAACGAAAGATATTAATCACTATAGAAACGAAAGTGAACCT	1133
Qy	1236	AGAACTCAGATTTTGAGCATCAAGAAAGTTTACCTCTGAGGATCTCAAGCGAGCTATGTC	1299
Db	1140	AGAACTCAGATTTTGAGCATCAAGAAAGTTTACCTCTGAGGATCTCAAGCGAGCTATGTC	1199
Qy	1296	TGTGATGCTAGAGTGCACAAAGCGCAAGTGCACAAAGACGCAAGGTGAAGCGCAAG	1353
Db	1200	TGTGATGCTAGAGTGCACAAAGCGCAAGTGCACAAAGACGCAAGGTGAAGCGCAAG	1257

```

RESULT 3
US-10-061-727-1
Sequence 1, Application US/10061727
Publication No. US20030170632A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Smith, Dirk E.
TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
FILE REFERENCE: 3151-A
CURRENT APPLICATION NUMBER: US/10/061,727
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 60/244,831
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2064
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2064)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (1792)..(1792)
OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro

```

US-10-061-727-1

Query Match	48.6%	Score 1047.8;	DB 15;	Length 2064;	
Best Local Similarity	99.8%;	Pred. No. 6.5e-216;			
Matches 1049;	Conservative	0;	Mismatches	2;	
		Indels	0;	Gaps	0;

QY	303	ATGACACTCTGTGTGTGTAGTAGTCTCTACTTTTATGGAAATCTCGAAAGTGAATGCC	362
Dp	1	ATGACACTCTGTGTGTGTAGTAGTCTCTACTTTTATGGAAATCTCGAAAGTGAATGCC	60
QY	363	TCGAAAGCTGCGCATGACTGTGGGACTGACACCACTGAGGGCAATCCCAAGTGTGAAGAT	422
Dp	61	TCGAAAGCTGCGCATGACTGTGGGACTGACACCACTGAGGGCAATCCCAAGTGTGAAGAT	120
QY	423	GAGCCAGCTGCGCATCAAGTGGCCCACTTTTGAACACTCTTGAATTTCAACTACAGACA	482
Dp	121	GAGCCAGCTGCGCATCAAGTGGCCCACTTTTGAACACTCTTGAATTTCAACTACAGACA	180
QY	483	GCCCATTCAGCTGGCCTTACTCTGATCTGTGTTATGGACTAAGCAGACCCGGACCTTGAG	542
Dp	181	GCCCATTCAGCTGGCCTTACTCTGATGTGTATGGACTAAGCAGACCCGGACCTTGAG	240
QY	543	GAGCCATTAACTTCCGCTCCCGGAAACCGACTTATGTAAGAGAAAGATGTCTGTGG	602
Dp	241	GAGCCATTAACTTCCGCTCCCGGAAACCGACTTATGTAAGAGAAAGATGTCTGTGG	300
QY	603	TTCCGCGCCCACTCTCTGAAATGACACTGGCACTATACCTGCATGTTAAGGAACACTACA	662
Dp	301	TTCCGCGCCCACTCTCTGAAATGACACTGGCAACACTATACCTGCATGTTAAGGAACACTACA	360
QY	663	TATTCGAGCAAAAGTGTGATTTCCCTTGGAAAGTTTTCAAAAGACAGCTGTTCAATTCC	722
Dp	361	TATTCGAGCAAAAGTGTGATTTCCCTTGGAAAGTTTTCAAAAGACAGCTGTTCAATTCC	420
QY	723	CCCATGAACTCCCACTGCAATAAACTGTATATGAAATATGGCACTTCAAGAGTCACTTGT	782
Dp	421	CCCATGAACTCCCACTGCAATAAACTGTATATGAAATATGGCACTTCAAGAGTCACTTGT	480
QY	783	CCAAATGTAGTGAATATTTTCCCTCCAGTGTCAACCCGACTATCACTGTGTATATGGGC	842
Dp	481	CCAAATGTAGTGAATATTTTCCCTCCAGTGTCAACCCGACTATCACTGTGTATATGGGC	540
QY	843	TGTTATAAAAATACGAAATTTTATATATGTAAATACCGAAGGTGAACCTTGCTCTC	902
Dp	541	TGTTATAAAAATACGAAATTTTATATATGTAAATACCGAAGGTGAACCTTGCTCTC	600
QY	903	ATTGSCCTAATTTCAAAATATATGGAATTAACAATGTGTGTTACATATCCGAAAGATGGA	962
Dp	601	ATTGSCCTAATTTCAAAATATATGGAATTAACAATGTGTGTTACATATCCGAAAGATGGA	660
QY	963	CGTACGTTTCACTCACACAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA	1022
Dp	661	CGTACGTTTCACTCACACAGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATGCA	720
QY	1023	GTGCCCCCTGTGATCCATTAACCTTAAGATCATGTGTCTATGGAAGAAAGAACCGAGAGAG	1082
Dp	721	GTGCCCCCTGTGATCCATTAAGATCATGTGTCTATGGAAGAAAGAACCGAGAGAG	780
QY	1083	GAGCTACTCAATCCCTGTACGGTCTATTTTATGTTTGTATGTAATCTGTGCAATGAGGTT	1142
Dp	781	GAGCTACTCAATCCCTGTACGGTCTATTTTATGTTTGTATGTAATCTGTGCAATGAGGTT	840
QY	1143	TGTGTGACCAATGTATGGAAGAAAGAACTGATGACATCATATGTGATGTGACATTAAGAA	1202
Dp	841	TGTGTGACCAATGTATGGAAGAAAGAACTGATGACATCATATGTGATGTGACATTAAGAA	900
QY	1203	AGTATAGTATAGTAAAGACAGAAAGATGAAACTGAACCTAGATTTTGAGCATCAAGAA	1262
Dp	901	AGTATAGTATAGTAAAGACAGAAAGATGAAACCAAGAACTAGATTTTGAGCATCAAGAA	960
QY	1263	GTTTATCTCTGAGGATCTCAAGCGGACGTAATGTCTGTCAATGTGTAAAGTGTCAAGGTGAA	1322
Dp	961	GTTTATCTCTGAGGATCTCAAGCGGACGTAATGTCTGTCAATGTGTAAAGTGTCAAGGTGAA	1020







Qy	78	CCAAAGTGTGAGATATTTTCCTTCAGGTGCAAAACGACATACCTTGATATGAGGC	842
Db	481	CCAAATGTGATGTGATATTTTCCTTCAGGTGCAAAACGACATACCTTGATATGAGGC	540
Qy	843	TGTTATAAATATACGAATTTTANTATATGTATATCCCAAGGTATGAACTTGATTTCTC	902
Db	541	TGTTATAAATATACGAATTTTANTATATGTATATCCCAAGGTATGAACTTGATTTCTC	600
Qy	903	ATTGCTTAATTTCCAAATATATGAAATATACATATGTGTGTTTACATATCCAGAAAATGGA	962
Db	601	ATTGCTTAATTTCCAAATATATGAAATATATACATATGTGTGTTTACATATCCAGAAAATGGA	660
Qy	963	CGTACGTTTCATCTCACGAGACTTGACTGTAAAGTATGAGGCTCTCCAAAAATGCA	102
Db	661	CGTACGTTTCATCTCACGAGACTTGACTGTAAAGTATGAGGCTCTCCAAAAATGCA	720
Qy	1023	GTGCCCCCTGTGATCATCATCACTATATCATGTGTGCTATGAGAAAGAACGAGAGAG	108
Db	721	GTGCCCCCTGTGATCATCATCACTATATCATGTGTGCTATGAGAAAGAACGAGAGAG	780
Qy	1083	GAGCTACTGATTTCCCTGTATAGGCTTAATTTAGTTTCTGATGATTTCCGATATGAGTT	114
Db	781	GAGCTACTGATTTCCCTGTATAGGCTTAATTTAGTTTCTGATGATTTCCGATATGAGTT	840
Qy	1143	TGATGACCAATTTGATGAGAAAGAAACCTGATGACATCATATTTGATGATGCAACATTAAGAA	120
Db	841	TGATGACCAATTTGATGAGAAAGAAACCTGATGACATCATATTTGATGATGCAACATTAAGAA	900
Qy	1203	AGTATAGTCATATGATGAAACAGAGATGAAAATGAACTCATGATTTTGAGATCAGAGAA	126
Db	901	AGTATAGTCATATGATGAAACAGAGATGAAAATGAACTCATGATTTTGAGATCAGAGAA	960
Qy	1263	GTTACTCTGAGAGATCTCAAGGCGAGGCTATGTCGTCACTGATGAGGCAAGGCGAA	132
Db	961	GTTACTCTGAGAGATCTCAAGGCGAGGCTATGTCGTCACTGATGAGGCAAGGCGAA	102
Qy	1323	GTTGCCAAAGCAGCCAGGCTGAGAGAGAAAG	1353
Db	1021	GTTGCCAAAGCAGCCAGGCTGAGAGAGAAAG	1051
RESULT 8			
US-10-282-162-41			
/ Sequence 41, Application US/10282162			
/ Publication No. US20030143697A1			
/ GENERAL INFORMATION:			
APPLICANT: REGENERON PHARMACEUTICALS, INC.			
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING			
TITLE OF INVENTION: AND USING			
FILE REFERENCE: REG 203-B-US			
CURRENT APPLICATION NUMBER: US/10/282,162			
CURRENT FILING DATE: 2002-10-28			
PRIOR APPLICATION NUMBER: 09/787,835			
PRIOR FILING DATE: 1999-09-22			
PRIOR APPLICATION NUMBER: PCT/US99/22045			
PRIOR FILING DATE: 1999-09-22			
NUMBER OF SEQ. ID NOS: 56			
/ SOFTWARE: FastSeq for Windows Version 3.0			
/ SEQ ID NO 41			
/ LENGTH: 2709			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
US-10-282-162-41			
Query Match 48.4%; Score 1043; DB 15; Length 2709;			
Best Local Similarity 99.5%; Pctd. No. Be-215;			
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0			
Qy	303	ATGACACTTCTGTGTGTGATGAGTCTCTACTTTATGGAATCTTGCAAGTGTATGCC	365
Db	1	ATGTGTCTTCTGTGTGTGATGAGTCTCTACTTTATGGAATCTTGCAAGTGTATGCC	60

QY	363	TCGAAGCTGCGCATCTACCTGGGGACATGACACATGAGGCAAAATCCAAAGTGTGGAAGAT	422
Db	61	TCGAAGCTGCGCATCTACCTGGGGACATGACACATGAGGCAAAATCCAAAGTGTGGAAGAT	120
QY	423	GAGCCAGCTGGCATCAAGTGGCCACTCTTGAACACTTCTTGAAATTCATACAGACA	482
Db	121	GAGCCAGCTGGCATCAAGTGGCCACTCTTGAACACTTCTTGAAATTCATACAGACA	180
QY	483	GCCATCTACGTGGCTTACTCTGATCTGATTTGATGATGAGACCGGAGCCTTGAG	542
Db	181	GCCATCTACGTGGCTTACTCTGATCTGATTTGATGATGAGACCGGAGCCTTGAG	240
QY	543	GAGCCATTAATCTTCCGCTCCCCGAGAACCGCATTTAGTAAGAAAAGATGTGCTGTG	602
Db	241	GAGCCATTAATCTTCCGCTCCCCGAGAACCGCATTTAGTAAGAAAAGATGTGCTGTG	300
QY	603	TTCCGGCCCACTCTCTCAATGACATCGGCAACTATCTGACATGTTAAGAAACATACA	662
Db	301	TTCCGGCCCACTCTCTCAATGACATCGGCAACTATCTGACATGTTAAGAAACATACA	360
QY	663	TATTGACAGAAAGCTGCATTTCCCTTGAAAGTTGTTCAAAAAGACAGCTGTTCATTC	722
Db	361	TATTGACAGAAAGCTGCATTTCCCTTGAAAGTTGTTCAAAAAGACAGCTGTTCATTC	420
QY	723	CCCATGAACTCCCACTGATATAACCTGATATAGAAATGTCATTCAGAGATCACTGT	782
Db	421	CCCATGAACTCCCACTGATATAACCTGATATAGAAATGTCATTCAGAGATCACTGT	480
QY	783	CCAAATGTATGATGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGTGTATGAGC	842
Db	481	CCAAATGTATGATGATATTTTCTTCCAGTGTCAAAACCGCATATCACTTGTGTATGAGC	540
QY	843	TGATATAAATACAGAAATTTTATATATATATACCCGAGGTAGAACTGATTCCTC	902
Db	541	TGATATAAATACAGAAATTTTATATATATATACCCGAGGTAGAACTGATTCCTC	600
QY	903	ATTGCTTAATTTCAATATATGAAATTAACAATGTGTGTTACATATCCAGAAAATGGA	962
Db	601	ATTGCTTAATTTCAATATATGAAATTAACAATGTGTGTTACATATCCAGAAAATGGA	660
QY	963	CGTAGCTTCACTCTACACGAGACCTGTGACTGTAAAGTAGAGGCTCTCCAAAATATGA	1022
Db	661	CGTAGCTTCACTCTACACGAGACCTGTGACTGTAAAGTAGAGGCTCTCCAAAATATGA	720
QY	1023	GTGCCCCCTGTGATCCATTCACCTATATCATGTGTGTCTATGAAAGAACCGAGAGAG	1082
Db	721	GTGCCCCCTGTGATCCATTCACCTATATCATGTGTGTCTATGAAAGAACCGAGAGAG	780
QY	1083	GAGCTACTAATCCCTGTACGGCTCATATTTAGTTTCTGATGATCTCTCCGATGAGGTT	1142
Db	781	GAGCTACTAATCCCTGTACGGCTCATATTTAGTTTCTGATGATCTCTCCGATGAGGTT	840
QY	1143	TGATGACCATTTGATGAAAAAAACCTGATGACATCATATGATGACACATTAACGA	1202
Db	841	TGATGACCATTTGATGAAAAAAACCTGATGACATCATATGATGACACATTAACGA	900
QY	1203	AGTATATGATCATATGTAAGAAACGAAATGAAATCTGAAATCTCAGATTTGAGATCAAGAA	1262
Db	901	AGTATATGATCATATGTAAGAAACGAAATGAAATCTGAAATCTCAGATTTGAGATCAAGAA	960
QY	1263	GTTAACCTGAGAGATCTCAAGCGACGATCTGTGATGCTGAAATGTGCAAGGCGAA	1322
Db	961	GTTAACCTGAGAGATCTCAAGCGACGATCTGTGATGCTGAAATGTGCAAGGCGAA	1022
QY	1323	GTTCGCAAAAGCCCAAGGTGAAGAGAAAG	1353
Db	1021	GTTCGCAAAAGCCCAAGGTGAAGAGAAAG	1051

Db 721 GTGCCCCCTGTGATTCATTCACCTAATGATCATGTGCTATGAGAAAGAACGAGAG 780  
Qy 1083 GAGCTACTCATTCCTCTGACGGCTGATTTTCTGAGATTTCTCGAATGAGGTT 1142  
Db 781 GAGCTACTCATTCCTCTGACGGCTGATTTTCTGAGATTTCTCGAATGAGGTT 840  
Qy 1143 TGTGAGACCATTTGAGAAAAAAGCTGATGACATCACTATTGATGTCCATTAGCAA 1202  
Db 841 TGTGAGACCATTTGAGAAAAAAGCTGATGACATCACTATTGATGTCCATTAGCAA 900  
Qy 1203 AGTATTAATCATAGTAGAACAAGAGTAATCTGAACTGATTTTGAAGATTAAGAA 1262  
Db 901 AGTATTAATCATAGTAGAACAAGAGTAATCAAGAACTGATTTTGAAGATTAAGAA 960  
Qy 1263 GTTACCTGTGAGGATCTGACGAGGCTATGTCTGTATGATAGAGGCAAGGCAA 1322  
Db 961 GTTACCTGTGAGGATCTGACGAGGCTATGTCTGTATGATAGAGGCAAGGCAA 1020  
Qy 1323 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1353  
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1051  
RESULT 10  
US-10-840-138-11  
; Sequence 11, Application US/10840138  
; Publication No. US20040224893A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Li-Hsien  
; APPLICANT: Lin, Hsin-Chieh  
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia  
; FILE REFERENCE: REG 207A  
; CURRENT APPLICATION NUMBER: US/10/840,138  
; CURRENT FILING DATE: 2004-05-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-840-138-11  
Query Match 48.4%; Score 1043; DB 18; Length 2709;  
Best Local Similarity 99.5%; Pred. No. 8e-215;  
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 303 ATGACACTTCTGTGTGTAGTAGTCTCTACTTTATGGAATCTGCAAGTATGCC 362  
Db 1 ATGTGCTCTCTGTGTGTAGTAGTCTCTACTTTATGGAATCTGCAAGTATGCC 60  
Qy 363 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 422  
Db 61 TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAAATCCAAAGTGTGAAGAT 120  
Qy 422 GAGCCAGCTCGCATGAAGGCCACTCTTTGAACACTTTGAAATTCATACAGACACA 482  
Db 121 GAGCCAGCTCGCATGAAGGCCACTCTTTGAACACTTTGAAATTCATACAGACACA 180  
Qy 483 GCCCATTCAGCTGGCTTACTCTGATCTGTGATTTGAGCTTAAGCAGACCGGAGACTTGAG 542  
Db 181 GCCCATTCAGCTGGCTTACTCTGATCTGTGATTTGAGCTTAAGCAGACCGGAGACTTGAG 240  
Qy 543 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAAGGAAAGATGTGTGG 602  
Db 241 GAGCCAAATTAATTCGCGCTCCCGAGAACCGCATTAAGTAAGGAAAGATGTGTGG 300  
Qy 603 TTCCGGCCCACTCTCTCATGACACTGGCAACTATACCTGATGTTAAGAAACACTACA 662  
Db 301 TTCCGGCCCACTCTCTCATGACACTGGCAACTATACCTGATGTTAAGAAACACTACA 360  
Qy 663 TATTGACGAAAGTTCATTTCCCTTGAAGTGTTCAAAAAGAAAGCTGTTCAATCC 722

Db 361 TATTGACGAAAGTTCATTTCCCTTGAAGTGTTCAAAAAGAAAGCTGTTCAATCC 420  
Qy 723 CCCATGAACCTCCAGTGCATTAACCTGATATGAAATATGCAATTCAGAGATCACTTGT 782  
Db 421 CCCATGAACCTCCAGTGCATTAACCTGATATGAAATATGCAATTCAGAGATCACTTGT 480  
Qy 783 CCAATGTATGATGATTTTCTTCCTTCAGGTGCAACCGCATATACCTTGTGATATGAGG 842  
Db 481 CCAATGTATGATGATTTTCTTCCTTCAGGTGCAACCGCATATACCTTGTGATATGAGG 540  
Qy 843 TGTATTAATATCAGATTTTATATATGATATACCCAGAGATTAACCTTGAGTTCCCTC 902  
Db 541 TGTATTAATATCAGATTTTATATATGATATACCCAGAGATTAACCTTGAGTTCCCTC 600  
Qy 903 ATTGCTTAATTTCAATTAATGAAATTAACATGTGTTTATCAATTCAGAAATATGCA 962  
Db 601 ATTGCTTAATTTCAATTAATGAAATTAACATGTGTTTATCAATTCAGAAATATGCA 660  
Qy 963 CGTACCTTCATCTCACCAGGACTGCTGCTGTAAGAGTAGTAGGCTCCCAAAAATGCA 1022  
Db 661 CGTACCTTCATCTCACCAGGACTGCTGCTGTAAGAGTAGTAGGCTCCCAAAAATGCA 720  
Qy 1023 GTGCCCCCTGTGATTCATTCACCTATATGATCATGTGCTATGAGAAAGAACGAGAG 1082  
Db 721 GTGCCCCCTGTGATTCATTCACCTATATGATCATGTGCTATGAGAAAGAACGAGAG 780  
Qy 1083 GAGCTACTCATTCCTCTGACGGCTGATTTTCTGAGATTTCTCGAATGAGGTT 1142  
Db 781 GAGCTACTCATTCCTCTGACGGCTGATTTTCTGAGATTTCTCGAATGAGGTT 840  
Qy 1143 TGTGAGACCATTTGAGAAAAAAGCTGATGACATCACTATTGATGTCCATTAGCAA 1202  
Db 841 TGTGAGACCATTTGAGAAAAAAGCTGATGACATCACTATTGATGTCCATTAGCAA 900  
Qy 1203 AGTATTAATCATAGTAGAACAAGAGTAATCTGAACTGATTTTGAAGATTAAGAA 1262  
Db 901 AGTATTAATCATAGTAGAACAAGAGTAATCAAGAACTGATTTTGAAGATTAAGAA 960  
Qy 1263 GTTACCTGTGAGGATCTGACGAGGCTATGTCTGTATGATAGAGGCAAGGCAA 1322  
Db 961 GTTACCTGTGAGGATCTGACGAGGCTATGTCTGTATGATAGAGGCAAGGCAA 1020  
Qy 1323 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1353  
Db 1021 GTTGCCAAAGCAGCCCAAGGTGAAGCAGAAAG 1051  
RESULT 11  
US-10-840-138-13  
; Sequence 13, Application US/10840138  
; Publication No. US20040224893A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Li-Hsien  
; APPLICANT: Lin, Hsin-Chieh  
; TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Neointimal Hyperplasia  
; FILE REFERENCE: REG 207A  
; CURRENT APPLICATION NUMBER: US/10/840,138  
; CURRENT FILING DATE: 2004-05-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-840-138-13  
Query Match 48.4%; Score 1043; DB 18; Length 2709;  
Best Local Similarity 99.5%; Pred. No. 8e-215;  
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 303 ATGACACTTCTGTGTGTAGTAGTCTCTACTTTATGGAATCTGCAAGTATGCC 362



Db 661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCCAAAAATGCA 720  
Qy 1023 GTGCCCCCTGATCATCTTACCTATATGATCATGTGTCATATGAGAAAGAACCCGAGAG 1082  
Db 721 GTGCCCCCTGATCATCTTACCTATATGATCATGTGTCATATGAGAAAGAACCCGAGAG 780  
Qy 1083 GAGCTACTCATCTCCCTGATGAGGCTCTATTTTATTTTCTGATGATGATTCCTGCAATGAGTT 1142  
Db 781 GAGCTACTCATCTCCCTGATGAGGCTCTATTTTATTTTCTGATGATGATTCCTGCAATGAGTT 840  
Qy 1143 TGGTGGACCATTTGATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1202  
Db 841 TGGTGGACCATTTGATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 900  
Qy 1203 AGTATTAAGTCATAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1262  
Db 901 AGTATTAAGTCATAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 960  
Qy 1263 GTTACCTCTGAGGATCTCAAGCGCACTATGTCTGCTATGCTAGAGTGCAGAAAGCGAA 1322  
Db 961 GTTACCTCTGAGGATCTCAAGCGCACTATGTCTGCTATGCTAGAGTGCAGAAAGCGAA 1020  
Qy 1323 GTTGCAGAAAGCAAGGCTGAGGAGCAAG 1353  
Db 1021 GTTGCAGAAAGCAAGGCTGAGGAGCAAG 1051

RESULT 13  
US-09-935-868-27  
Sequence 27, Application US/09935868  
Patent No. US20020164690A1  
GENERAL INFORMATION:  
APPLICANT: Regeneron Pharmaceuticals, Inc  
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
FILE REFERENCE: REG 203D  
CURRENT APPLICATION NUMBER: US/09/935, 868  
CURRENT FILING DATE: 2002-04-11  
PRIOR APPLICATION NUMBER: PCT/US99/22045  
PRIOR FILING DATE: 1999-09-22  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 27  
LENGTH: 2733  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(2730)  
US-09-935-868-27

Query Match 48.4%; Score 1043; DB 9; Length 2733;  
Best Local Similarity 99.5%; Pred. No. 8, 1e-215;  
Matches 1046; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 303 ATGACACTTCTGTGTGTGTAGTGTCTCTACTTTTATGGAATCTGCAAGTATGCC 362  
Db 1 ATGTGTCTTCTGTGTGTGTAGTGTCTCTACTTTTATGGAATCTGCAAGTATGCC 60  
Qy 363 TGAAGACGCTGCGAGTACTGGGGAATAGACACCAAGAGGCAAAATCCAGTGTGGAAT 422  
Db 61 TGAAGACGCTGCGAGTACTGGGGAATAGACACCAAGAGGCAAAATCCAGTGTGGAAT 120  
Qy 423 GAGCAGACTCGCATCAAGTGCACCTCTTGAACACTCTTGAATCACTACAGACA 482  
Db 121 GAGCAGACTCGCATCAAGTGCACCTCTTGAACACTCTTGAATCACTACAGACA 180  
Qy 483 GCCCATTCAGTGGCTTACTCTGATCTGTGATTTGATGAGTAAAGAGACGAGACCTTGAG 542  
Db 181 GCCCATTCAGTGGCTTACTCTGATCTGTGATTTGATGAGTAAAGAGACGAGACCTTGAG 240  
Qy 543 GAGCAGTAACTTCCGCTCTCCGAGAACCGCATTAATTAAGGAGAAAGATGTGCTGG 602

Db 241 GAGCAGTAACTTCCGCTCTCCGAGAACCGCATTAATTAAGGAGAAAGATGTGCTGG 300  
Qy 603 TTCCGGCCCACTCTCTCTCATATGACATGCGCACTATACCTGATGTTAAGAACTACA 662  
Db 301 TTCCGGCCCACTCTCTCTCATATGACATGCGCACTATACCTGATGTTAAGAACTACA 360  
Qy 663 TATTGAGCAAAAGTTCATTTCCCTTGAAGTTGTCAAAAGACAGCTGTTTCAATTCC 722  
Db 361 TATTGAGCAAAAGTTCATTTCCCTTGAAGTTGTCAAAAGACAGCTGTTTCAATTCC 420  
Qy 723 CCCATGAAGTCCCACTGATTAAGTATATGATATGATATGATGATGATGATGATGATGATGAT 782  
Db 421 CCCATGAAGTCCCACTGATTAAGTATATGATATGATATGATGATGATGATGATGATGATGAT 480  
Qy 783 CCAATATGATGATGATATTTTCTCTTCCAGTGTCAAACCGCATATCACTTGTATATGAGCC 842  
Db 481 CCAATATGATGATGATATTTTCTCTTCCAGTGTCAAACCGCATATCACTTGTATATGAGCC 540  
Qy 843 TGTATTAATAATACGAATTTTAT 902  
Db 541 TGTATTAATAATACGAATTTTAT 600  
Qy 903 ATTGCTTAATTTCAATATATGAAATTAACATGTGTTTATATATATATATATATATATATAT 962  
Db 601 ATTGCTTAATTTCAATATATGAAATTAACATGTGTTTATATATATATATATATATATATAT 660  
Qy 963 CGTACGTTTCATCTCACCAGGACTCTGATGTTAAAGTGTGAGTCTCCCAAAATGCA 1022  
Db 661 CGTACGTTTCATCTCACCAGGACTCTGATGTTAAAGTGTGAGTCTCCCAAAATGCA 720  
Qy 1023 GTGCCCCCTGATCATCTTACCTATATGATGATGATGATGATGATGATGATGATGATGATGAT 1082  
Db 721 GTGCCCCCTGATCATCTCACCAGGACTCTGATGTTAAAGTGTGAGTCTCCCAAAATGCA 780  
Qy 1083 GAGCTACTCATCTCCCTGATGAGGCTCTATTTTATTTTCTGATGATGATTCCTGCAATGAGTT 1142  
Db 781 GAGCTACTCATCTCCCTGATGAGGCTCTATTTTATTTTCTGATGATGATTCCTGCAATGAGTT 840  
Qy 1143 TGGTGGACCATTTGATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1202  
Db 841 TGGTGGACCATTTGATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 900  
Qy 1203 AGTATTAAGTCATAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1262  
Db 901 AGTATTAAGTCATAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 960  
Qy 1263 GTTACCTCTGAGGATCTCAAGCGCACTATGTCTGCTATGCTAGAGTGCAGAAAGCGAA 1322  
Db 961 GTTACCTCTGAGGATCTCAAGCGCACTATGTCTGCTATGCTAGAGTGCAGAAAGCGAA 1020  
Qy 1323 GTTGCAGAAAGCAAGGCTGAGGAGCAAG 1353  
Db 1021 GTTGCAGAAAGCAAGGCTGAGGAGCAAG 1051

RESULT 14  
US-10-287-035-27  
Sequence 27, Application US/10287035  
Publication No. US20030104567A1  
GENERAL INFORMATION:  
APPLICANT: Neil Stahl and George D. Yancopoulos  
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
FILE REFERENCE: REG 203DA  
CURRENT APPLICATION NUMBER: US/10/287, 035  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: USSN 09/935, 868  
PRIOR FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: USSN 09/787, 835  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: USSN 09/313, 942  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 09/313, 942







Mon Dec 27 15:31:10 2004

us-08-917-710-1.rnrm

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 25, 2004, 12:59:51; Search time 8168 Seconds  
(Without alignments)  
10698.709 Million cell updates/sec

Title: US-08-917-710-1  
Perfect score: 2155  
Sequence: 1 CGGTGGCGCCGCTTAGAA.....CTAAAAAAAAAAAAAAAAAAAA 2155

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 44308572 seqs, 2027541865 residues

Total number of hits satisfying chosen parameters: 88617144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing filter 45 summaries

Database:

```
1: Pending Patents NA Main: *
2: /cgn2_6/ptodata/1/pna/PCRN2_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/PCRN2_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US082_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US083_COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US084_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US085_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US086_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US087_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US088_COMB.seq.*
14: /cgn2_6/ptodata/1/pna/US089_COMB.seq.*
15: /cgn2_6/ptodata/1/pna/US090_COMB.seq.*
16: /cgn2_6/ptodata/1/pna/US091_COMB.seq.*
17: /cgn2_6/ptodata/1/pna/US092_COMB.seq.*
18: /cgn2_6/ptodata/1/pna/US093_COMB.seq.*
19: /cgn2_6/ptodata/1/pna/US093B_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US093B_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US094_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US095_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US095B_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US095C_COMB.seq.*
25: /cgn2_6/ptodata/1/pna/US095D_COMB.seq.*
26: /cgn2_6/ptodata/1/pna/US096_COMB.seq.*
27: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US096C_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*
31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*
32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*
33: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US098A_COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US098B_COMB.seq.*
36: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US098D_COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*
39: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US099D_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US099E_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US099F_COMB.seq.*
44: /cgn2_6/ptodata/1/pna/US099G_COMB.seq.*
45: /cgn2_6/ptodata/1/pna/US100A_COMB.seq.*
46: /cgn2_6/ptodata/1/pna/US100B_COMB.seq.*
47: /cgn2_6/ptodata/1/pna/US101A_COMB.seq.*
48: /cgn2_6/ptodata/1/pna/US101B_COMB.seq.*
49: /cgn2_6/ptodata/1/pna/US102A_COMB.seq.*
50: /cgn2_6/ptodata/1/pna/US102B_COMB.seq.*
51: /cgn2_6/ptodata/1/pna/US103A_COMB.seq.*
52: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
53: /cgn2_6/ptodata/1/pna/US104A_COMB.seq.*
54: /cgn2_6/ptodata/1/pna/US104B_COMB.seq.*
55: /cgn2_6/ptodata/1/pna/US105A_COMB.seq.*
56: /cgn2_6/ptodata/1/pna/US105B_COMB.seq.*
57: /cgn2_6/ptodata/1/pna/US106A_COMB.seq.*
58: /cgn2_6/ptodata/1/pna/US107A_COMB.seq.*
59: /cgn2_6/ptodata/1/pna/US107B_COMB.seq.*
60: /cgn2_6/ptodata/1/pna/US107C_COMB.seq.*
61: /cgn2_6/ptodata/1/pna/US108A_COMB.seq.*
62: /cgn2_6/ptodata/1/pna/US108B_COMB.seq.*
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq.*
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq.*
65: /cgn2_6/ptodata/1/pna/US6000_COMB.seq.*
66: /cgn2_6/ptodata/1/pna/US6001_COMB.seq.*
67: /cgn2_6/ptodata/1/pna/US6002_COMB.seq.*
68: /cgn2_6/ptodata/1/pna/US6003_COMB.seq.*
69: /cgn2_6/ptodata/1/pna/US6004_COMB.seq.*
70: /cgn2_6/ptodata/1/pna/US6005_COMB.seq.*
71: /cgn2_6/ptodata/1/pna/US6006_COMB.seq.*
72: /cgn2_6/ptodata/1/pna/US6007_COMB.seq.*
73: /cgn2_6/ptodata/1/pna/US6008_COMB.seq.*
74: /cgn2_6/ptodata/1/pna/US6009_COMB.seq.*
75: /cgn2_6/ptodata/1/pna/US6010_COMB.seq.*
76: /cgn2_6/ptodata/1/pna/US6011_COMB.seq.*
77: /cgn2_6/ptodata/1/pna/US6012_COMB.seq.*
78: /cgn2_6/ptodata/1/pna/US6013_COMB.seq.*
79: /cgn2_6/ptodata/1/pna/US6014_COMB.seq.*
80: /cgn2_6/ptodata/1/pna/US6015_COMB.seq.*
81: /cgn2_6/ptodata/1/pna/US6016_COMB.seq.*
82: /cgn2_6/ptodata/1/pna/US6017_COMB.seq.*
83: /cgn2_6/ptodata/1/pna/US6018_COMB.seq.*
84: /cgn2_6/ptodata/1/pna/US6019_COMB.seq.*
85: /cgn2_6/ptodata/1/pna/US6020_COMB.seq.*
86: /cgn2_6/ptodata/1/pna/US6021_COMB.seq.*
87: /cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
88: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq.*
89: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq.*
90: /cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
91: /cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
92: /cgn2_6/ptodata/1/pna/US6026_COMB.seq.*
93: /cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
94: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*
95: /cgn2_6/ptodata/1/pna/US6029_COMB.seq.*
96: /cgn2_6/ptodata/1/pna/US6030_COMB.seq.*
97: /cgn2_6/ptodata/1/pna/US6031_COMB.seq.*
98: /cgn2_6/ptodata/1/pna/US6032_COMB.seq.*
99: /cgn2_6/ptodata/1/pna/US6033_COMB.seq.*
100: /cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
101: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
102: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*
103: /cgn2_6/ptodata/1/pna/US6037_COMB.seq.*
104: /cgn2_6/ptodata/1/pna/US6038_COMB.seq.*
105: /cgn2_6/ptodata/1/pna/US6039_COMB.seq.*
106: /cgn2_6/ptodata/1/pna/US6040_COMB.seq.*
107: /cgn2_6/ptodata/1/pna/US6041_COMB.seq.*
108: /cgn2_6/ptodata/1/pna/US6042_COMB.seq.*
109: /cgn2_6/ptodata/1/pna/US6043_COMB.seq.*
110: /cgn2_6/ptodata/1/pna/US6044_COMB.seq.*
111: /cgn2_6/ptodata/1/pna/US6045_COMB.seq.*
112: /cgn2_6/ptodata/1/pna/US6046_COMB.seq.*
113: /cgn2_6/ptodata/1/pna/US6047_COMB.seq.*
114: /cgn2_6/ptodata/1/pna/US6048_COMB.seq.*
115: /cgn2_6/ptodata/1/pna/US6049_COMB.seq.*
116: /cgn2_6/ptodata/1/pna/US6050_COMB.seq.*
```

**This Page Blank (uspio)**